

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:44:38 ; Search time 44 Seconds  
(without alignments)  
1626.938 Million cell updates/sec

Title: US-10-782-570-2  
Perfect score: 3906  
Sequence: 1 MNQNNNEYELIDSKNSYP.....PFTNHTKNTLNIEATNYDID 744

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1159	29.7	1180	2 A26858	parasporal crystal
2	1158	29.6	1180	2 I39870	parasporal crystal
3	923.5	23.6	934	2 B29838	parasporal crystal
4	819	21.0	1136	1 US8S8I	parasporal crystal
5	710	18.2	659	2 S10228	parasporal crystal
6	695	17.8	652	2 I39811	parasporal crystal
7	692	17.7	1138	2 A48944	parasporal crystal
8	676	17.3	1160	2 I40589	parasporal crystal
9	659.5	16.9	1157	1 S49247	parasporal crystal
10	630.5	15.9	652	2 A27323	parasporal crystal
11	611	15.6	1228	2 S00873	parasporal crystal
12	588.5	15.1	719	2 I39815	insecticidal prote
13	585.5	15.0	719	2 I39815	insecticidal prote
14	585.5	15.0	719	2 S25383	parasporal crystal
15	578	14.8	649	1 JH0261	parasporal crystal
16	576	14.7	1165	2 S11446	parasporal crystal
17	573	14.7	1178	1 USBSXH	parasporal crystal
18	563.5	14.4	719	2 I40590	parasporal crystal
19	560.5	14.3	1177	2 A49785	crv465 protein -
20	551	14.1	1154	2 S39536	parasporal crystal
21	540.5	13.8	1171	2 A37829	parasporal crystal
22	540.5	13.8	1171	2 I40572	parasporal crystal
23	538	13.8	1176	2 S32649	parasporal crystal
24	534.5	13.7	1176	2 A48970	parasporal crystal
25	528	13.5	618	2 S11445	parasporal crystal
26	526.5	13.5	655	2 JCT140	protoxin - Bacillu
27	522.5	13.4	823	2 S04181	parasporal crystal
28	519.5	13.3	1174	2 A42459	parasporal crystal
29	517.5	13.2	1160	2 S32647	parasporal crystal

ALIGNMENTS

RESULT 1

A26858  
Parasporal crystal protein cry4Aa1 - Bacillus thuringiensis subsp. israelensis  
N:Alternate names: parasporal crystal protein cryIVA  
C:Species: Bacillus thuringiensis subsp. israelensis  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 05-Oct-2004  
C:Accession: A26858; S48691  
R:Ward, E.S.; Ellar, D.J.  
Nucleic Acids Res. 15, 7195, 1987  
A:Title: Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding  
A:Reference number: A26858; MUID:88015571; PMID:2821500  
A:Accession: A26858  
A:Molecule type: DNA  
A:Residues: 1-1180 <VAR>  
A:Cross-references: UNIPROT:P16480; UNIPARC:UPI000016EA42; GB:Y00423; NID:940351; PIDN:C  
A:Note: the authors translated the codon GCA for residue 308 as Thr  
F:Nishimoto, T.; Yoshisue, H.; Ihara, K.; Sakai, H.; Komano, T.  
FEBS Lett. 348, 249-254, 1994  
A:Title: Functional analysis of block 5, one of the highly conserved amino acid sequence  
A:Reference number: S48691; MUID:94307434; PMID:7913448  
A:Accession: S48691  
A:Molecule type: DNA  
A:Residues: 667-676 <NIS>  
A:Cross-references: UNIPARC:UPI000017819A  
C:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 29.7%; Score 1159; DB 2; Length 1180;  
Best Local Similarity 37.3%; Pred. No. 1.2e-64;  
Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;

Qy	5	NNNEYELIDS--KNLSYPSNRNIDHSVPYTNPNQPLQNTNYKEWLNMCQNTQYGDNF	62
Db	6	NKNSEYELNASKKLNISNN----YTRYPIENSPKQLLSQNTYKDWLNMCQNTQYGDNF	61
Qy	63	ETFSADDTIAAVSAGTIVSGTLLAGIGLTSISGFIGIGAIISFGTLITVFPAGSQD	122
Db	62	ETFDIDS---GELSAVTIVGVTLTGFGFTT----PLGL---ALIGFGTLIPVLPAPQDQS	111
Qy	123	KTVMTQIFKGEIIFVDPTLTESI KQLKQLTLEGFRQLQSNTALDDWRKUKRLQAPGLP	182
Db	112	NT-MSDFITQTKNIKKELASTYISNANKILNRSFNIVISTYHNHLKTWE-----NNPNPQ	165
Qy	183	PSSALQQAALTLKTRFENVHDFIREIP--GFQLETYKTLTLLPIYAQANFHLNLLQQA	240
Db	166	NTQDVRTQIQLVHVFQNVIPDELVNSCPNPSDDCYNINLVSSVAQANLHLTVLNQAV	225
Qy	241	ELADEWNADIHPSQIEPNAGTSDDYIKLLKENIPKYSNYCANTYREGINKLRNEP-----	295
Db	226	KFEAYLKNRQFDYLEP-LPTAIDYYPVLTKAIEDYTNVCVTTYKGLNLKTTTPDSNLD	284
Qy	296	-NMRWSIFNRRYMTITVLDITIAQFSFYDIKRYKDSIGRIGGIKTELTRITYTTEINF	354





Db 575 PNNIIPDLKYEFYKDPFPAIDAVPMLSSLNQLITIAIQPLNMTSNNQVIIDRIEIPIT 634  
QY 704 SSYRQNRKQKLEFIQKINTFTNTHTKNTLNIETATYDID 744  
Db 635 QSVLDETNQNLSEREVNVNALTNDKDALNIGTTDYDID 675  
RESULT 5  
S10228  
Parasporal crystal protein cry3Ba1 - Bacillus thuringiensis (fragment)  
N/Alternate names: coleopter-an-active parasporal crystal protein; delta-endotoxin  
C/Species: Bacillus thuringiensis  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 05-Oct-2004  
C/Accession: S10228  
R/Sick, A.; Gaertner, F.; Wong, A.  
Nucleic Acids Res. 18, 1305, 1990  
A/Title: Nucleotide sequence of a coleopter-an-active toxin gene from a new isolate of Ba  
A/Reference number: S10228; MUID:90206811; PMID:2320431  
A/Accession: S10228  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-659 <SIC>  
A/Cross-references: UNIPROT:P17969; UNIPARC:UPI0000126C13; EMBL:X17123; NID:g40258; PIDN:  
C/Genetics:  
C/Gene: cryIIIB  
C/Superfamily: Parasporal crystal protein  
C/Keywords: delta-endotoxin; toxin  
Query Match 18.2%; Score 710; DB 2; Length 659;  
Best Local Similarity 28.9%; Pred. No. 7.9e-37;  
Matches 217; Conservative 115; Mismatches 270; Indels 148; Gaps 31;  
QY 1 MNQNNNEYIID-SKNLSYPSNRNIDHSRYPTNNPNQPLNTNYKEWLNMCQNTQYG 59  
Db 9 MNPNNRSEYDIKVTNPSELPTN-----HNQYPLADPNPNSTLEELNYKEFLRMTADNST-- 62  
QY 60 DNPETASADTTAAVSGAGTIVSGTLGAGIGLTSISGPIGIIAIIISFGTLITVFWPAG 119  
Db 63 ---EVLDSSTVKDVGTVGIVSVQILGVVG-----VPPAGALTSTFYQSFLNALWPS- 110  
QY 120 EQDKTVMTQFIKMGEIFVDTPLTESIKQLKLTLEGFQILQSYNTALDDWRKLRLOAP 179  
Db 111 --DADPWKAFMAQVEVLIDKKIEYAKSKALAEQLQNNFEDYVNALDSWKK----- 161  
QY 180 GLPSSALQAALTLKIRFENVHDFIREIPGFQLETYKTLPLPIYAQAANFHLNLQOG 239  
Db 162 -APVNLRSQDRIRLELFSQAESHFRNMPSPFAVSKFVLFLPTYAQAANTHLLLLKOA 220  
QY 240 AELADEWNADIHPISOIEPNAGTSD--YYKLLKENIPKYSNCANTYREGLNKLRNEPN 296  
Db 221 QVFGEEGWY-----SSEDAEFYQRLKLTQYTDHCVMNVNVLNLSRGSTY 268  
QY 297 MRWSIENDRYRYMTITVLDTIAQSFYDIKRYKDSIGRIGIKTELTRREIYTTIEINPDL 356  
Db 269 DAWVKFNRRFREMFTLVLDLIVLFPFYDVRLYSK-----GVKTELTRDIFTDPI-FTLN 321  
QY 357 TYLEIOPNLAIMENYLRSGRLFSFLDELIFYTK-----NETYGNRLVGIANR 405  
Db 322 ALQEGYGTFFSIENSIRKP--HLFDYLRGIEFHTLRPGYSGKDSFNWWSGNY---VETR 376  
QY 406 NRSTYATGTTEIYGERGTPPTTKLIPFESYKVSIVTDROV--TPTSPPN--IYFTIN 461  
Db 377 PSIGSNDTITSPFYGDKSIEPIQK--LSFDGQKVY-----RTIANTDIAAFPDDKIYFGVT 430  
QY 462 QIBLYLNNSPSNKL---TYSA-----GGNLNDK---KTTDFQFPVKOCKPIINPNC 508  
Db 431 KVPFSQYDDQKNETSTQTYDSKRYNGYLGQAQSDIDQLPPEITD--EPLK----- 478  
QY 509 LPSYNSYSHILSQSLFNYSYKIGLALNILYTGALGTHSSVNRNNAISDKIITMIPAK 568  
Db 479 -----AYSHQNLNAECFLMDQRGTI--PPFT-----WTHRSVDFFNTIDAEKITQLPVPK 527  
QY 569 GNSLDTNSKVIEGPGHTGGNLVLYQ-----SQGRLEITCRTFNSQTQSYIRLRATNGAGN 624

Db 528 AYALSSGASIIIEGPGFTGCGNLFLKSSNSIAKPKVTLNSAALLQRYRVIRVAST--- 583  
QY 625 TLPNLSLTIPGVIGIPPPQLNNTFSGTNVNNIYQ--GDFGY--FQPPSTVTTLPLNRNIPP 680  
Db 584 --TNLRLFV-----QNSNNDFLVIYINKMTNIDGDLTYQTFDPATS-----NSNMGF 628  
QY 681 IFNRAD-----VSNLSILIIDKIEFIPI 702  
Db 629 SGGTNDFTIIGAESFVSNKIIYIDKIEFIPV 658  
RESULT 6  
I39811  
Parasporal crystal protein cry3Bb1 - Bacillus thuringiensis  
N/Alternate names: parasporal crystal protein cryIIIB2  
C/Species: Bacillus thuringiensis  
C/Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Oct-2004  
C/Accession: I39811  
R/Donovan, W.P.; Ruper, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burks, M.C.; Johnson, T.B.  
Appl. Environ. Microbiol. 58, 3921-3927, 1992  
A/Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal crys  
A/Reference number: I39811; MUID:93119147; PMID:1476436  
A/Accession: I39811  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-652 <RES>  
A/Cross-references: UNIPROT:Q06117; UNIPARC:UPI0000126C14; GB:M89794; NID:g142729; PIDN:  
C/Genetics:  
C/Gene: cryIIIB2  
C/Superfamily: Parasporal crystal protein  
Query Match 17.8%; Score 695; DB 2; Length 652;  
Best Local Similarity 28.4%; Pred. No. 6.8e-36;  
Matches 209; Conservative 121; Mismatches 286; Indels 120; Gaps 28;  
QY 1 MNQNNNEYIIDSKNLSYPSNRNIDHSRYPTNNPNQPLNTNYKEWLNMCQ-GNTQYG 59  
Db 1 MNPNNRSEHDTI---KVTNPSELQTNHQYPLADPNPNSTLEELNYKEFLRMTDSSTVL 57  
QY 60 DNPETASADTTA-AVSGATIVSGTLGAGIGLTSISGPIGIIAIIISFGTLITVFWPA 118  
Db 58 DN-----STVKDAVGTGIVSVQILGVVG-----VPPAGALTSTFYQSFLANTWPS 102  
QY 119 GSQDKTVMTQFIKMGEIFVDTPLTESIKQLKLTLEGFQILQSYNTALDDWRKLRLOA 178  
Db 103 ---DADPWKAFMAQVEVLIDKKIEYAKSKALAEQLQNNFEDYVNALSWKK----- 153  
QY 179 PGLPSSALQAALTLKIRFENVHDFIREIPGFQLETYKTLPLPIYAQAANFHLNLQOG 238  
Db 154 --TPLSLRSKRSQDRIRLELFSQAESHFRNMPSPFAVSKFVLFLPTYAQAANTHLLLLKD 211  
QY 239 GAELADEWNADIHPISOIEPNAGTSDDYKLLKENIPKYSNCANTYREGLNKLRNEPNMR 298  
Db 212 AQVFGEEGWY-----SEDAEFYHQLKLT-QQYTDHCVMNVNVLNGLRGSTYDA 262  
QY 299 WSIENDRYRYMTITVLDTIAQSFYDIKRYKDSIGRIGIKTELTRREIYTTIEINPDLTY 358  
Db 263 WVKFNRRFREMFTLVLDLIVLFPFYDIRLYSK-----GVKTELTRDIFTDPI-PSLNTL 315  
QY 359 LBIQNLAIMENYLRSGRLFSFLDELIFYTK-----NETYGNRLVGIANRNR 407  
Db 316 QEVGTPFTLSIENSIRKP--HLFDYLRGIEFHTLRPGYSGKDSFNWWSGNY---VETRPS 370  
QY 408 STYATGTTEIYGERGTPPTTKLIPFESYKVSIVTDROV--TPTSPPN--IYFTINQI 463  
Db 371 IGSSKTTITSPFYGDKSTEVQK--LSFDGQKVY-----RTIANTDIAAAMPNGKYLGVTKV 424  
QY 464 ELYLNNSPSNKL---TYSA---GGNLNDKTTDFQFPVKOCKPIINPNCPLPSYNSYSH 517  
Db 425 DFSQYDDQKNETSTQTYDSKRYNGYHVAQSDTD--QLPPEITDDEPL-----EKAYSH 474  
QY 518 ILSQFSLEFNYSYKIGLALNILYTGALGTHSSVNRNNAISDKIITMIPAKGNSLDTNSK 577



Db 475 QLNVAECFLMODRGTI--PFPT----WTHRSVDFNTIDAETQLPFWKAYALSSGAS 528  
Qy 578 VIEGPGHTGGLVYLQ-----SOGLEITCRPNSTQSYIRLRVATNGAGNTLPLNISLTI 633  
Db 529 IIEGPGTGGNLLFLKSSNSIAKFKVTLNSAALLQRYVRIRVAST-----TNLRLFV 582  
Qy 634 PGVIGIPQRLNNTFTGNYN-----NLQYGFYGFYFPSTVTLPLNRNPIPFNRAD 686  
Db 583 -----QNSNDFLVIYINKTNKDDLLTYQTFDLATTNSNMFGSDKNELIIGAESF 634  
Qy 687 VNSILIIDKIEFIP 702  
Db 635 VSNEKIYIDKIEFIPV 650

RESULT 7  
A48944  
Parasporal crystal protein cry7Aa1 - Bacillus thuringiensis  
N;Alternate names: parasporal crystal protein cryIIIC  
C;Species: Bacillus thuringiensis  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Oct-2004  
C;Accession: A48944  
R;Lambert, B.; Hofte, H.; Anyas, K.; Jansens, S.; Soetaert, P.; Peferoen, M.  
Appl. Environ. Microbiol. 58, 2536-2542, 1992  
A;Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silent activit  
A;Reference number: A48944; MUID:92384571; PMID:1514800  
A;Contents: B7S137J  
A;Accession: A48944  
A;Status: preliminary  
A;Molecule type: DNA; protein  
A;Residues: 1-1138 <LAM>  
A;Cross-references: UNIPROT:Q03749; UNIPARC:UPI000002C1E6; GB:M64478; NID:G142760; PIDN:  
A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBI:P:112093)  
C;Superfamily: Parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 17.7%; Score 692; DB 2; Length 1138;  
Best Local Similarity 28.3%; Pred. No. 2.4e-35;  
Matches 221; Conservative 127; Mismatches 288; Indels 146; Gaps 33;  
Qy 1 MNQNNNEYIIDSKNLSYPSNRNIDHS-RYPYTNPNQPLONTNYKSWLNMCQNTQYG 59  
Db 1 MNLNLDGYE-----DSNRITLNSLNYPTQKALSPLKNNYQDFLSITE-----R 46  
Qy 60 DNPETFASADTIAAVSAGTIIVSGTLLAGIGLTSISGPIGIGAIIS--FGTLITVFWP 117  
Db 47 EQPALASGNT--AINTVSVTGATLSA-----LGVPGASFITNFYKTAGLWMP 94  
Qy 118 AGEQDKTWTFQIKWGEIFVDTPLETESIKQLKLTLEGFRQILQSYNTALDDWRKLRQL 177  
Db 95 ---ENKIIDWFMEVEALIDQKIEEYVRNKAIAELDGLSALDKYQKALADW--LGKQD 149  
Qy 178 APGLPPSALQQAALTALKIRFENVHNDPIREIPGQLETKYTLPLPIYAQAANFHLNLLQ 237  
Db 150 DP-----EAILSTAFRIIDSLFEFSMPSEKVTGVEIPLLTVAQAANLHALLR 200  
Qy 238 QGAELADENADIHPSQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGINKLRNPNM 297  
Db 201 DSTLYGKNG--FTQNILEN-----YNRQKRISSEYDCHCTKWTNSGLRSLNGSTYE 251  
Qy 298 RWSIFNDYRRYMTITVLDITIAQFSFYDIKRYKDSIGRIGGIGKTELREIYITEINFDRLT 357  
Db 252 QWYNFRFRREMILMALDVLAVFPFHPDRYSME-----TSTQLTREYVTDPVSL-IS 304  
Qy 358 YLEIQPNLAIMEYNLTRSGLRFLSFLDELIPYT-KNETYGNRL-----VGIANR 405  
Db 305 NPDIGPSFSQMENTAIRTP-HLVYLDLXYTSKYKAFSHEIQPDLFYMSAHKVSFKKS 363  
Qy 406 NRSTVATTGTETIYXGERTGPPTTKTLIPFESYKYSIVTDROVTPSTSPNNIY-----FTI 460  
Db 364 EQSNLYTTG---LYGKTSG-----YISSGAYSFH-GNDIYRTLAAPSVVVPYTONYGV 413

Qy 461 NQIELY-----LNNSPENK--LTVSAGNLSNDKKTDFOPPVKCKOCPINPNCLPSYN 513  
Db 414 EQVEFYGVKHVYRGDNKYDLTVDSIDQLPPDGE-----PIHE 452  
Qy 514 SYSHILSQ-PSEFNYSYKIGLALNLTGALGTHSSVNRNNAISDKLITMIPAIGKNSL 572  
Db 453 KYTHRLCHATAIFKSTPDYDNATIPFS-----WTHRSAEYNNRIYPNKIKTIPAVOMYKL 508  
Qy 573 DTNSKVIEGPGHTGGLNVLVYLSQSGRLEITCRTPNS--TQSYIRLRVATNGAG--NTLPN 628  
Db 509 DDPSTVVKPGFTGGDLVKEGSTYIGDIKATVNSPLSQRYVRVATNVSGQFNYYIN 568  
Qy 629 ISLTIPGVIGIPQRLNNTFTSGT-----NWNLYQGFYGFYFPSTVTLPLNRNPIPFEN 683  
Db 569 DKIT-----LQTKFQNTVETIGEGKDLTYGSGFYIEYSTTIQFP-DEHPKITLH 616  
Qy 684 RADVS-NSILIIDKIEFIPITSSVRQNRKOKLETIOTKINTFTNTKNTLNTAENYD 742  
Db 617 LSDLSNNSSFYVDSIEFIPVDVNY---AEKEKLEKAKAVNTLFT-BGRNALQKDVTDYK 672  
Qy 743 ID 744  
Db 673 VD 674

RESULT 8  
I40589  
Parasporal crystal protein cry8Ca1 - Bacillus thuringiensis  
N;Alternate names: parasporal crystal protein cryIII  
C;Species: Bacillus thuringiensis  
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Oct-2004  
C;Accession: I40589  
R;Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asano  
Curt. Microbiol. 28, 15-19, 1994  
A;Title: Cloning, heterologous expression, and localization of a novel crystal protein  
A;Reference number: I40589; MUID:94100786; PMID:17764305  
A;Accession: I40589  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-1160 <RES>  
A;Cross-references: UNIPROT:Q45706; UNIPARC:UPI0000126CPE; EMBL:U04366; NID:G532523; PID  
C;Superfamily: Parasporal crystal protein  
C;Keywords: Delta-endotoxin

Query Match 17.3%; Score 676; DB 2; Length 1160;  
Best Local Similarity 27.7%; Pred. No. 2.5e-34;  
Matches 217; Conservative 122; Mismatches 317; Indels 128; Gaps 29;  
Qy 1 MNQNNNEYIIDSKNLSYPSNRNIDHSRYPYTNPNQPLONTNYKSWLNMCQ-NTQYG 59  
Db 1 MSPNNQNEYIIDALSPTSVDNSI---RYPLANDQNTLQNNMYKDYLKMTSTNAELS 57  
Qy 60 DNPETFASADTIAAVSAGTIIVSGTLLAGIGLTSISGPIGIGAIISFGTLITVFWPAG 119  
Db 58 RNPGTFTISAQ--AVGTGIDIVSTIISGLG-----IPVLGEVFSILGSLIGLLWPSN 107  
Qy 120 EQDKTWTFQIKWGEIFVDTPLETESIKQLKLTLEGFRQILQSYNTALDDWRKLRQLQAP 179  
Db 108 NEN--VWQIFPNRVEELIDQKILDSVRSRAIDLANSRIAVEYYQNALEDWRK----- 158  
Qy 180 GLPPSSALQQAALTALKIRFENVHNDPIREIPGQLETKYTLPLPIYAQAANFHLNLLQ 239  
Db 159 --NPHST--RSAALVKERFGNAELRTNMGSFQNTNYETPLPLTYAQAASLHLLVMRDV 214  
Qy 240 AELADENADIHPSQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGINKLRNPNMRW 299  
Db 215 QIYKKEWG---YPO-----NDIDLIFYKEQVSRYARSYDCHCVQYNAAGLNKLRGTAKQW 265  
Qy 300 SIFNDYRRYMTITVLDITIAQFSFYDIKRYKDSIGRIGGIGKTELREIYITEINFDRLT 357  
Db 266 VDNFRFRREMVMVLDLVALFPYVD-----ARIYPLETNAELTETIFDTPVG-----S 313  
Qy 358 YLEIQPNLAIMEYNLTRSGLRFLSFLDELI-----FYTKNETYGNRLVGIANRNRSTVATT 413

Db 314 YVTGQSSTLISWDMIPAAALPSFTLENLRLKDPDFTLQEI-----RWYTSFRON 364  
QY 414 GTIILIGERTGPTTKTLI---PPESYKVISVTRDQVTPSTP-----FPNIY 457  
Db 365 GTIEYNYMGQBLTLSIYIGSFFNKYSGLVLAGAEDIIPVGQNDIYRVVMYTIYGRYNSL 424  
QY 458 FTINQIELYLNNSFNSKLTYSAGNLNSDKKTTDFQFPVKCKOCKPIINPNCLPSYNSYSH 517  
Db 425 LGVNPVTFPSN--NQKIYSKPKQAGGKITDSGEELTYE-----NYQSYSH 471  
QY 518 ILSQFSLFNYSYKIGLALNLYTGALGWHSSHVNRNNAISDKIITMIPAIGNSLDTNSK 577  
Db 472 RVSYITSFBIKSTGGTVLGVV--PIFGWTHSSASRNFIYATKISQIPINKASR--TSGG 527  
QY 578 VI-----EGPHTGNGNLVYLOSQ-----RLEITCRTNSQSYVIRLRYATNGAGN-TLPN 628  
Db 528 AVNMFQGL--YNGGPMVKLGGSGSQVINLRFVATDAKASQRYRIRIYASDRAGKFTIS 586  
QY 629 ISLTIPGVIGIPQRLN--NTEFGTNYNNLQYDGFVQFPSTVTLPLNRPNIPIFNRAD 686  
Db 587 RSPENPATYSASTAYNTMSTNASLTYSTPAYAESG-----PINLIGSGSRTED 636  
QY 687 VS-----NSILIDKIEFIPITSSVRQNRKQKLETIQKINTFTNHTNKTNLIEATN 740  
Db 637 ISITKEAGANLYIDRIEPIPVNTLF---EAEBDLVAKKAVNGLFTNE-KDALQTSVTD 692  
QY 741 YDID 744  
Db 693 YQVN 696  
RESULT 9  
S49247  
parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis  
N;Alternate names: Parasporal crystal protein cryIH  
C;Species: Bacillus thuringiensis  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 05-Oct-2004  
C;Accession: A59350; S49247  
R;Lambert, B.; Buysse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.; V  
Appl. Environ. Microbiol. 62, 80-86, 1996  
A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity agai  
A;Reference number: A59350; MUID:96141404; PMID:8572715  
A;Accession: A59350  
A;Molecule type: DNA  
A;Residues: 1-1157 <LMS>  
A;Cross-references: UNIPROT:Q45733; UNIPARC:UPI000002F5A5; EMBL:Z37527; NID:g547554; PID  
A;Experimental source: serovar tolworthi  
C;Comment: This parasporal crystal protein, active against corn borer and other insects,  
C;Superfamily: Parasporal crystal protein  
C;Keywords: delta-endotoxin  
Query Match 16.9%; Score 659.5; DB 1; Length 1157;  
Best Local Similarity 27.1%; Pred. No. 2.7e-33;  
Matches 218; Conservative 118; Mismatches 298; Indels 171; Gaps 33;  
QY 1 MNQNNNEVEIIDSKNLSYPSNENIDHSRVPYTNPNQPLQNTNYKELNMCQNTQYGD 60  
Db 1 MNRNNQNEYIIDAPHCQPSD---DDVRYPLASDPAALQNNYKDYLOMT--DEDDYD 55  
QY 61 NF-ETFSADPTIAAVSAGITVSGTLLAGIGGLTISGPGIIGAIITISFQTLITVFWPAG 119  
Db 56 SYINPSLISIGRDAVQTALTVGRLGALG-----VPFSQIVSFYQFLLNTLWPV- 106  
QY 120 EQDKTWTQIKNGEIVFDPLTSTESIKQLKQLTLEGFROILOSYNALDDW-----RK 172  
Db 107 -NDTAIWEAFMRQVEELVNOQIITEFARNQALRQGLGDSFNYYQSRQLQNLADRNDTRN 165  
QY 173 LKELQAPGLPPSSALQQAALTAKIRENVHNDPIREIPGFOLEYTKTLTLLPIYAQAANEH 232  
Db 166 LSVVRA-----QFIADL-----DFVNAIPLFVANGQQVPLLSVTAQAVNLH 207  
QY 233 LNLLOQGAELADEWNADIHPSQIEPNAGTSDDDYYIKLLKENIPKYSNYCANTYREGLNKL 292

Db 208 LLLLDKASLFGSGWGF-----TQGEISTYDRQLELTAKYTNVCTWYNTGLDLRL 258  
QY 293 NEPNRWISFNDRYRYMTITVLDTIAQSFYDIKRYKDSIGRIGGKIKTLTRIYYTEIN 352  
Db 259 GTNTESWLRYHQFRREMTLVLVDVVALFPYIVRLYPT-----GSNPQLTREVVDPV 312  
QY 353 FD-----RLTYLEIQ-----PNLAIMEYNLRTSGURL---PSFLDELIF 388  
Db 313 FPPPNVGLCRWGTNPYNTFSELENAFIRPHLPDLRLNSLTSSNRPVSSNFMFYWSG 372  
QY 389 YTKNETYGNRLV-----GIANNRSTY--ATTGTEIYYGERTGPPPTTKTLIPFESYKVS 440  
Db 373 HTLRSYLNDSAVQEDSYGLITTTTRATINPGVDGTNRI-----ESTAVDFRSALIG 423  
QY 441 IVTRQVTPSTPFPNIYFTINQIELYLNNSPNKLTYSAGNLNSDKKTTDFQFPVKKDC 500  
Db 424 IY-----GYNRASFPVPGLFNG---TTS---PANGGC 449  
QY 501 KPIINPNC-LP---SYNSYSHILSQFSLFNYSYKIGLALNLYVTGALG---WTHSSVNRN 553  
Db 450 ROLYDNDLDELPPDESTGSTRHLSHVTFP--SFQTNQAGSIANAGSVPTVWTRRDVNL 507  
QY 554 NAISDKIITMIPAIGNSLDTNSKVIIEGFGHTGGNLVYLSQ---GRLEITCRTPNSTQS 610  
Db 508 NTITPNRITQLPLVKASAPVSGTTLVKPGFTGGILRRRTTNGTFTGLRVTVNSP-LTQ 566  
QY 611 YYIRLRYATNGAGNLTPLNISL-TIPGVIGIPQRLNNTFTSGTNYNNLQYDGFYQFPST 669  
Db 567 YRLRVFASTG-----NFSIRVLRGGVSGIDVRLGSTMN--RGOELTYESFTTREF--T 616  
QY 670 VTPLNRPNIPIFNRAVDSNSI-----LIIDKIEFIPITSSVRQNRKQKLETIQ 719  
Db 617 TTGPNP--PFTTQAEILTVNAGSVTGGYYIDRIEIVPNPA---REAEEDLEAAK 671  
QY 720 TKINTFFTNHTKNTNLNIEATNYDID 744  
Db 672 KAVASLFT-RTRDGLQVNVTDYQVD 695  
RESULT 10  
A27323  
parasporal crystal protein cry3Aa1 - Bacillus thuringiensis  
N;Alternate names: Coleopteran-specific insect control protein; crystal protein cryC; del  
C;Species: Bacillus thuringiensis  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 05-Oct-2004  
C;Accession: A27323; A26853; A29987; A28407; S60781; I39813  
R;Herrnstadt, C.; Gillyoy, T.E.; Sobieski, D.A.; Bennett, B.D.; Gaertner, F.H.  
Gene 57, 37-46, 1987  
A;Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active del  
A;Reference number: A27323; MUID:88112860; PMID:2828180  
A;Accession: A27323  
A;Molecule type: DNA  
A;Residues: 1-652 <HER>  
A;Cross-references: UNIPROT:Q9SGN9; UNIPARC:UPI00000AEBDC; GB:M22472; NID:gl42733; PIDN:f  
A;Experimental source: strain San Diego  
R;Hoefte H.; Seurinck, J.; Van Houtven, A.; Vaecck, M.  
Nucleic Acids Res. 15, 7193, 1987  
A;Title: Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus thuri  
A;Reference number: A26853; MUID:88015559; PMID:3658680  
A;Accession: A26853  
A;Molecule type: DNA  
A;Residues: 9-652 <HOE>  
A;Cross-references: UNIPARC:UPI000002B8CD; GB:Y00420; NID:g40252; PIDN:CAA68482.1; PID:g4  
A;Experimental source: var. tenebrionis  
R;McPherson, S.A.; Perlak, F.J.; Fuchs, R.L.; Marrone, P.G.; Lavrik, P.B.; Fischhoff, D.f  
Bio/Technology 6, 61-66, 1988  
A;Title: Characterization of the coleopteran-specific protein gene of Bacillus thuringier  
A;Reference number: A29987  
A;Accession: A29987  
A;Molecule type: DNA  
A;Residues: 9-652 <MCP>  
A;Cross-references: UNIPARC:UPI000002B8CD

A;Experimental source: var. tenebrionis  
 R;Sekar, V.; Thompson, D.V.; Maroney, M.J.; Bookland, R.G.; Adang, M.J.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 7036-7040, 1987  
 A;Title: Molecular cloning and characterization of the insecticidal crystal protein gene  
 A;Reference number: A28407  
 A;Accession: A28407  
 A;Molecule type: DNA  
 A;Residues: 9-652 <SEK>  
 A;Cross-references: UNIPARC:UPI000002B8CD  
 A;Experimental source: var. Tenebrionis  
 R;Adams, L.F.; Mathewes, S.; O'Hara, P.; Petersen, A.; Guertler, H.  
 Mol. Microbiol. 14, 381-389, 1994  
 A;Title: Elucidation of the mechanism of CryIIIA overproduction in a mutagenized strain  
 A;Reference number: S60781; MUID:95131759; PMID:7830581  
 A;Accession: S60781  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 9-652 <ADA>  
 A;Cross-references: UNIPARC:UPI000002B8CD; EMBL:U10985; NID:G506182; PIDN:AA43266.1; PIDN:AA43266.1; PIDN:AA43266.1  
 A;Experimental source: var. tenebrionis strain NB176, a mutant of strain NB125  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994  
 R;Wu, S.J.; Dean, D.H.  
 J. Mol. Biol. 255, 628-640, 1996  
 A;Title: Functional significance of loops in the receptor binding domain of Bacillus thuringiensis  
 A;Reference number: S62317; MUID:96163559; PMID:8568902  
 A;Contents: annotation  
 R;Donovan, W.P.; Gonzalez, J.M.  
 Mol. Gen. Genet. 214, 365-372, 1988  
 A;Title: Isolation and characterization of EG2158, a new strain of Bacillus thuringiensis  
 A;Reference number: I39812; MUID:89112139; PMID:3146015  
 A;Accession: I39812  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 9-652 <RES>  
 A;Cross-references: UNIPARC:UPI000002B8CD; GB:H37207; NID:G142735; PIDN:AAA50255.1; PIDN:AAA50255.1; PIDN:AAA50255.1  
 A;Experimental source: strain EG2158  
 R;Reixeira De Souza, M.; Lecadet, M.M.; Lereclus, D.  
 J. Bacteriol. 175, 2952-2960, 1993  
 A;Title: Full expression of the cryIIIA toxin gene of Bacillus thuringiensis requires a  
 A;Reference number: I39813; MUID:93259939; PMID:8491716  
 A;Accession: I39813  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 9-58 <RES>  
 A;Cross-references: UNIPARC:UPI00000B007B; GB:L03393; NID:G304150; PIDN:AAA22350.1; PIDN:AAA22350.1; PIDN:AAA22350.1  
 A;Experimental source: UNIPARC:UPI00000B007B  
 A;Gene: cryIIIA  
 A;Superfamily: Parasporeal crystal protein  
 C;Keywords: delta-endotoxin

Query Match 15.9%; Score 620.5; DB 2; Length 652;  
 Best Local Similarity 26.9%; Pred. No. 3.2e-31;  
 Matches 198; Conservative 109; Mismatches 302; Indels 127; Gaps 28;  
 QY 1 MNQNNNEYBII-DSKNLSPVSRNIDHSRYPTNNPNQPLNTNYKEWLNCCQNTQYG 59  
 DB 9 MNPNNRSEHDTIKTENNEVPTN---HVQYPLAETNPPTLDLNYKEFLRWTDN--- 60  
 QY 60 DNPETASADTIAVSAAGTVSGTLLAGISGSLTISGPIGIIAIIISFGTLITVFWPAG 119  
 DB 61 -NTEALDSSTTKDVIQKISVGVGDLGVG-----PPFG--GALVSVFTNFLTNIWPSE 111  
 QY 120 EOKTVMTQFKMGEIFVDVPTLESIKQLKLTLEGFRQLQSNTALDDWRKLRLOAP 179  
 DB 112 DP-----WKAFWEQVEALMDQKIADYAKNKAELQGLQNNVEDYVSALSSWQK----- 160  
 QY 180 GLPPSSALQQAALTITKIRFENVHNDFTREIPGQLETKYTLTLLPIYAQAANFHLNLLQOG 239  
 DB 161 -NPVSSRNPHSQGRIRLFPSQAESHFRNSMPSFAISGYEVLFTLTYYAQAANTHLLKDA 219  
 QY 240 AELADEW---NADTHPSQIEPNAGTSDDYVYKLLKENIPKYSNYCANTYREGIAKLIRNEP 296  
 DB 220 QIYGEENGWYKEBID-----AEFYKROLKLTQETDHCVKVYVGLDKLRGSSY 267

QY 297 MRWSIFNDYRRYMTITVLDITIAQSFYDIKRYKDSIGRIGGIKTELFRBIYTTTEINFDR 356  
 DB 268 ESMVFNRYRRENTLVLDLIALFLYDVRYPKE-----VKTELTRDVLTDPI----- 316  
 QY 357 TYLEIQPNLAIMEYNLTRSGL-----RLFSFLDELIFYTKNET--YGNRLVGIAINR 407  
 DB 317 ----VGYN-NLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYGVNSDFNWSGNY 371  
 QY 408 -STVATTG-----TEIYGBRTGPTTKTLIPES-YKVSIVTDROVTPSPFNIFTI 460  
 DB 372 VSTRPSIGSNDIITSPYGNKSEPVQNFGEKVRVAVANTNLAWPSA-----VTSGV 427  
 QY 461 NQIELYLNNSPSNKL---TYSAGNLSNDKTTDFQPPVKCKDCKPIINPNCLPSYNSYSH 517  
 DB 428 TKVEFSQYNDQTDSEASTQTYDSKRVGAVSWDSIDQLPPTTDEPLEK----- 475  
 QY 518 ILSQFSLPNYSYKIGLALNLTLYGALG-----WTHSSVNRNNAISDKIITWIPAIKNS 571  
 DB 476 -----GYSHQLNVMCFMQSGRTIPVLWTWTHKSVDFNMIDSKKITQLPLVKAYK 527  
 QY 572 LDTNSKVIIEGPGHTGNNLVYLSQGRLEITCRTP--NSTQSYIIRLAYATNGAGNTLPNI 629  
 DB 528 LQSGASVAGPRTGGDIIOCTENGSAATIVTPDVSYSKYRARIHYASTS-----QI 581  
 QY 630 SLTIPGVIGIPORLANNFTSGTNYN---NLQYGDGFGYFQFPFSTVTLPLNRNIPFIRNAD 686  
 DB 582 TETL-SLDGAP---FNQYYPDKTINKGDTLYNSFNLSASTPELSGN-NLQIGVTGLS 636  
 QY 687 VNSIILIIKIEFIP 702  
 DB 637 AGDKV-YIDKIEFIPV 651

## RESULT 11

S00873

Parasporeal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
 N;Alternate names: parasporeal crystal protein cryA4  
 C;Species: Bacillus thuringiensis subsp. thuringiensis  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-Oct-2004  
 C;Accession: S00873  
 R;Brizzard, B.L.; Whiteley, H.R.  
 Nucleic Acids Res. 16, 2723-2724, 1988  
 A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus  
 A;Reference number: S00873; MUID:88203216; PMID:3362680  
 A;Accession: S00873  
 A;Molecule type: DNA  
 A;Residues: 1-1228 <BRI>  
 A;Cross-references: UNIPROT:P05517; UNIPARC:UPI0000126BDC; EMBL:X06711; NID:G40264; PIDN:  
 C;Genetics:  
 A;Gene: cryA4  
 A;Start codon: TTG  
 A;Superfamily: Parasporeal crystal protein  
 C;Keywords: delta-endotoxin

Query Match 15.6%; Score 611; DB 2; Length 1228;  
 Best Local Similarity 26.2%; Pred. No. 3.3e-30;  
 Matches 210; Conservative 113; Mismatches 294; Indels 184; Gaps 35;  
 QY 1 MNQNNNEYBIIIDSKNLSYPSNRNIDHSRYPTNNPNQPLNTNYKEWLNCCQNTQYGD 60  
 DB 1 MTSNRKNNEIINA-----VSNHSAQMDLLP-----DARIEDSLCIAEGN----- 40  
 QY 61 NPEETASADTIAVSAAGTVSGTLLAGISGSLTISGPIGIIAIIISFGTLITVFWPAGE 120  
 DB 41 NIDPFVSAST---VQTGINIAGRILGVIG-----VPPAGQLASFSYFVGLWELWRGR 89  
 QY 121 QDKTVMTQFKMGEIFVDVPTLESIKQLKLTLEGFRQLQSNTALDDWRKLRLOAP 180  
 DB 90 DQ---WEIFLEHVQLINQIITENARTALARLQGLGDSFRAYQOSLEDMLE-----NRDD 142  
 QY 181 LPSSSALQQAALTITKIRFENVHNDFTREIPGQLETKYTLTLLPIYAQAANFHLNLLQOGA 240

Db 143 ARTSRVLYTQYIALEL-----DFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDAS 195  
Qy 241 ELADENNADHPQIEPNAGTSD--YYKLLKENIPKYSNYCANTYRGLNKLNRPENM 297  
Db 196 LFGSEFGL-----TSQEIQRYYERQVTRDYSYDVCVYNTGLNSLRGTAA 243  
Qy 298 RWSIFNDYRRYMTITVLDITIAQSFYDIKRYKDSIGRIGGIKT-----TEIN 352  
Db 244 SWRYNQPRDLGLVLDLVALPSPYDTRYPIN-----TSQALREYVTDIGAATGVN 297  
Qy 353 FDLRT-YLEIQPNLAIMEYNLRSGLRFLPSFLDEL-IF-----YTKNETYGN 397  
Db 298 MASGMWYNNAPSAIAEAAIRSP-HLLDFLEQLAIFGASSRWSNTRHMYWRGHTIQS 356  
Qy 398 RLVGIANRRTSYATTGTTEIYGERTPPT-----TKTLIPFESYKYSIVTDROVTPSP 453  
Db 357 RPIG-GLGANTSTHGATNTSI-----NPVTLRPSARDVYRTESYAGVLLMGYILEPIHG 409  
Qy 454 PNIYFTINQIELYLNNSPKLTVSAGGNLSNDKTTDFOFPVK-----KCKPPIPN 507  
Db 410 PTVRFNF-----TNPN-----ISDRGTANYSQPYESGLQLKDSETLPPE 451  
Qy 508 CL--PSYNSYSHLSQSLFNYSYKIGLALNI-LYTGALGWTSHSVNRNNAISDKIITMI 564  
Db 452 TTERPNYESYSHLSHIGIILQS-----RVNVPVYS-----WTHRSADRTNTIGPNRITQI 502  
Qy 565 PAIKGNSLDTNSKVIKSGHGTGNLYVLSQSQ-----GRLEITCRTPNSTQSYIIRLYAT-- 619  
Db 503 PMVKASLPQGTTVVRPGPGTGGDILRRNTTGGFGPIRVTVNGP-LTORYRIGFRYASTV 561  
Qy 620 -----NGAGNTLPNISLTIPGVIGIPQORLNTTSGTNNLYQDGFYGFQFPSTVTL 673  
Db 562 DFDFFVSRGGTTVNNFRF-----LRTWNSG-----DELKYNFVRRAFTT----- 601  
Qy 674 LNRNPIPFNR-ADV-----SNSILIIDKIEPIPTSSVRQNRKQKLETIQTKIN 723  
Db 602 -----PFTFTQIIDIIRTSIQGLSGNGEVYIDKIEIIPVTATPEAYD---LERAQEA 653  
Qy 724 TPTNTNKTNLNTEATNYDID 744  
Db 654 ALFTNTPRRLKTDVTDYHID 674

RESULT 12  
I39815  
insecticidal protein cryV - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C>Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Oct-2004  
C:Accession: I39815  
R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
Appl. Environ. Microbiol. 59, 1683-1687, 1993  
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for  
iensis subsp. kurstaki.  
A:Reference number: I39815; MUID:93298009; PMID:8517758  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45752; UNIPARC:UPI0000036008; GB:M98544; NID:g142767; PIDN:  
C:Genetics:  
C:Gene: cryV  
C:Superfamily: Parasporal crystal protein

Query Match 15.1%; Score 588.5; DB 2; Length 719;  
Best Local Similarity 26.1%; Pred. No. 3.9e-29;  
Matches 207; Conservative 112; Mismatches 293; Indels 181; Gaps 34;

Qy 15 KNLSPSNRNDH-SRYPYTNPNQPLQNTNYKEWLNMCQNTQYQDGFETASADTIAA 73  
Db 8 KHQSFSSNAKVDKISTDSLKNETDIELQNIHSDCLM-----SEY-ENVEPFPVASTIQ- 61  
Qy 74 VSAGTIVSGTLLAGIGLTSISGPIG--IGAILISFGTLITVFWPAGEQDKVTWTFQIK 131

Db 62 -----TGIGIAGKILGTGLVPPAGQVASLYSIFLGBLWPKG---KNQWEIPME 106  
Qy 132 MGEIFVDPTLTESIQLKLOTLLEGFRQILOSNTALDDW---RKLKRLQAPGLPPSSALQ 188  
Db 107 HVEEIIQKISTYARNKALTDLKGGLDALAVYHDSLESWVGVRNNTRAR-----SVVK 159  
Qy 189 QAALTLLKIRFENVHNDFIREFIOPLETYKTLPIYAQAANFHLNLLCOGAEADENNA 248  
Db 160 SQYIALEM-----FVQKLPSPAVSGEEVPLLPYQAANLHLLLRDASIFGKENG- 211  
Qy 249 DIHPSQIEPNAGTSDYYKLLKENIPKYSNYCANTYRGLNKLNRPENMNRSIFNDYRY 308  
Db 212 -LSSSEI-----STFYNRQVERAGDYSCHVKVYSTGLNLRGTNAESWRYNQFRRD 263  
Qy 309 MTITVLDITIAQSFYDIKRYKDSIGRIGGIKT--ELTREIYYTEI-----NFDLRT-Y 358  
Db 264 MTLMWLDLVALPSPYDQWYP-----IKTQAQLTREYVTDIGAIVPHPSFTSTTWY 315  
Qy 359 LEIQPNLAIMEYNLRSGLRFLPSFLDELIFYT-----KNETYGN-----RLVGIAN 404  
Db 316 NNNAISPSAIEAAVVRNP-HLLDFLEQVTIYLSLRWSNTQYNNMGGHKLBFRTIG-GT 373  
Qy 405 RNRSTYATTGTTEIYGERTPPTTKLIPFES---YKVSIVTDROVTPSP---FPNIYF 458  
Db 374 LNISTQGSTNTSI-----NPVT---LPFTSRDVTRESLAGLNLFLTQPVNGVPRVDF 423  
Qy 459 TINQIELYLNNSPKLTVSAGGNLSNDKTTDFOFPVKCKPPIPNCLPSYNSYSHI 518  
Db 424 ---HWKFVTHPIASNFYYPGVAGITQIQDSENELPPEATGQ-----PNYESYSHR 472  
Qy 519 LSQSLFNYSYKIGLALNITYTGALGWTSHSVNRNNAISDKIITMIPAIKGNSLDTNSKV 578  
Db 473 LSHIGLISASHKALVYS-----WTHRSADRTNTIEPNSITQIPLVKAFNLSSGA 524  
Qy 579 IEGPGHGTGNLYVLSQSQ-----RLEITCRTPNSTQSYIIRLYAT-----NGAG 623  
Db 525 VRGPGTGGDILRRNTTGTGDIRVNI---NPPAQRYVRIRYASTTDLQPHTSINGKA 581  
Qy 624 NTLPLNLSLTIPGVIGIPQORLNTTSGTNNLYQDGFYGFQFPSTVTLPLNRNIFIN 683  
Db 582 INQGNFSATM-----NRGEDLDYKTFRTVGFTT-----PFSP- 613  
Qy 684 RADVNSILI-----IDKIEPIPTSSVRQNRKQKLETIQTKINTFTNHTK 731  
Db 614 -LDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAYD---FEKAQEKVTLFTSTNP 669  
Qy 732 NTLNTEATNYDID 744  
Db 670 RGLKTDVKDYHID 682

RESULT 13  
I39814  
insecticidal protein cryVI - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C>Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Oct-2004  
C:Accession: I39814  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I39814  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPARC:UPI0000036009; GB:L36338; NID:g540281; PIDN:AAC36999.1; PID:  
C:Genetics:  
C:Gene: cryVI  
C:Superfamily: Parasporal crystal protein

Query Match 15.0%; Score 585.5; DB 2; Length 719;  
Best Local Similarity 26.1%; Pred. No. 6e-29;



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Job time : 48 secs

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634 ---SGDEVYIDKIEFIPM 648



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:47:28 ; Search time 47 Seconds  
(without alignments)  
1308.738 Million cell updates/sec

Title: US-10-782-570-2

Perfect score: 3906

Sequence: 1 MNQNNNEVEIIDSKNLSYP.....FFTHTKNTLNIEATNYDID 744

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCITUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1153	29.5	1180	2	US-09-224-024-28
2	1153	29.5	1180	4	PCT-US94-07902-28
3	900	23.0	686	2	US-09-224-024-31
4	900	23.0	686	4	PCT-US94-07902-31
5	791.5	20.3	1169	1	US-08-315-468-4
6	710	18.2	651	1	US-08-315-468-6
7	710	18.2	651	2	US-07-941-650A-4
8	710	18.2	659	2	US-08-996-441B-112
9	710	18.2	659	2	US-08-993-722A-112
10	710	18.2	659	2	US-08-993-170A-112
11	710	18.2	659	2	US-08-993-775B-112
12	710	18.2	659	2	US-09-427-770-112
13	710	18.2	659	2	US-09-427-769-112
14	704	18.0	652	2	US-08-996-441B-110
15	704	18.0	652	2	US-08-993-722A-110
16	704	18.0	652	2	US-08-993-170A-110
17	704	18.0	652	2	US-08-993-775B-110
18	704	18.0	652	2	US-09-377-466B-4
19	704	18.0	652	2	US-09-427-770-110
20	704	18.0	652	2	US-09-427-769-110
21	704	18.0	652	2	US-10-232-665-4
22	704	18.0	652	4	PCT-US92-00040-2
23	697	17.8	652	2	US-09-377-466B-6
24	697	17.8	652	2	US-10-232-665-6
25	695	17.8	652	2	US-08-996-441B-4
26	695	17.8	652	2	US-08-996-441B-10
27	695	17.8	652	2	US-08-996-441B-28

28 695 17.8 652 2 US-08-996-441B-44 Sequence 44, Appl  
29 695 17.8 652 2 US-08-996-441B-68 Sequence 68, Appl  
30 695 17.8 652 2 US-08-996-441B-98 Sequence 98, Appl  
31 695 17.8 652 2 US-08-996-441B-111 Sequence 111, Appl  
32 695 17.8 652 2 US-08-993-722A-4 Sequence 4, Appl  
33 695 17.8 652 2 US-08-993-722A-10 Sequence 10, Appl  
34 695 17.8 652 2 US-08-993-722A-28 Sequence 28, Appl  
35 695 17.8 652 2 US-08-993-722A-44 Sequence 44, Appl  
36 695 17.8 652 2 US-08-993-722A-68 Sequence 68, Appl  
37 695 17.8 652 2 US-08-993-722A-98 Sequence 98, Appl  
38 695 17.8 652 2 US-08-993-722A-111 Sequence 111, Appl  
39 695 17.8 652 2 US-08-993-170A-4 Sequence 4, Appl  
40 695 17.8 652 2 US-08-993-170A-10 Sequence 10, Appl  
41 695 17.8 652 2 US-08-993-170A-28 Sequence 28, Appl  
42 695 17.8 652 2 US-08-993-170A-44 Sequence 44, Appl  
43 695 17.8 652 2 US-08-993-170A-68 Sequence 68, Appl  
44 695 17.8 652 2 US-08-993-170A-98 Sequence 98, Appl  
45 695 17.8 652 2 US-08-993-170A-111 Sequence 111, Appl

## ALIGNMENTS

RESULT 1  
US-09-224-024-28  
; Sequence 28, Application US/09224024  
; Patent No. 6056953  
; GENERAL INFORMATION:  
; APPLICANT: Leslie Hickie  
; APPLICANT: Jewel Payne  
; TITLE OF INVENTION: Materials and Methods for the Control of  
; TITLE OF INVENTION: Calliphoridae Pests  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/224,024  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/856,226  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA79  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1180 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-224-024-28

Query Match 29.5%; Score 1153; DB 2; Length 1180;  
Best Local Similarity 37.2%; Pred. No. 6.4e-89;  
Matches 282; Conservative 131; Mismatches 282; Indels 64; Gaps 25;

Qy 5 NNNEYEIDS--KNLSYPSNRNIDHSRYPYTNPNPQPLQNTNYKEWLNMCQNTQYGDNF 62

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Db      6 NKNEYETLNASQKLNISNN-----YRPIENSPKQLQSTNYKDWLNWCQQOQYGGDF 61
QY      63 ETPASADTTAAVSAAGTIVSGTLAGIGLTSISGPIGIIIGAIISFGTLITVFWPAGEQD 122
Db      62 ETPIDS---GELSAITVVGTLTGFGFTT---PLGL---ALIGFTLIPVLFPQAQDOS 111
QY      123 KTVMTQPIKNGEIVFDVTPLETESIKQLQTLQLEGFRQILOSYNTALDDWRKLKELQAPGLP 182
Db      112 NT-WSDFITQTKNIIKKEIASTYISNANKILNRSFNVIYHNHLKTWE-----NNPNPQ 165
QY      183 PSSALQQAALTLKIRFENVHNDIREIP--GFQLETYKTLILLPIYAQAANFHLNLQOQA 240
Db      166 NTQDVRTQIQLVHYHFQNVIPELVNSCPNPSDCDYNNILVSSYAQAANHLTVLNQAV 225
QY      241 ELADENADIHPSQIEPNAGTSDDYKLLKENIPKYSNYCANTYRGLNKLNEP-----295
Db      226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTKAIEDYTNVCVTTYKGLNLKTTDPSNLD 284
QY      296 -NMRWSIENDRYRMYTITVLDITIAQSFYDIKRYKDSIGRIGIKTELTRREIYTTINPD 354
Db      285 GNINWNTYRTKMTTAVLDLVALFPNYDVGKPI-----GVQSELTRREIYQV-LNFE 337
QY      355 RLTYLEIOPNLAIMBYNLTGRSLRFLSFLDELIFFTKNETYGNRLVGIANRNRSTYA---411
Db      338 ESPYKY--DFQYQEDSLTRP-HLFTWLDLSNFYEKAQTTNNPF-TSHYNMFHYTLDN 393
QY      412 TTGTEIIGERTGPPPTKTLIPESYKVSIVTDQVTPSPPNYIYFTINQIELYLNNSP 471
Db      394 ISQKSSVFGNNHVTDKLSL--GLATNIYIFLLNVISLDNKYLDNNYSKMDFFITNGT 451
QY      472 ---SNKLTYSAGNLNDKKTTFQFPVKDCKPIINPNCLPSYNSHILSQFSLFNY- 527
Db      452 RLLEKELT-AGSQIITYDVNKNIFGLPILKPRENQAIPFTFYDNYSHILSFIKSLSP 510
QY      528 -SYKIGLALNLYTGALGWTSHSSVNRNNAISDKIITMIPAIGNSLDTNSKVIEGFGHTG 586
Db      511 ATYK-----TQVYTF--WTHSSVDPKNTIYTHLTQIPAVKANSIGTASKKVQVGFHTG 563
QY      587 GNLVYLQSQGRLEICTRTNSTQSYIRLRYATNGAGNTLPNLSLTIPGVIGIPPORLNN 646
Db      564 GDLI--DPKDFKITCOHSNFQOQSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620

RESULT 2
PCT-US94-07902-28
; Sequence 28, Application PC/TUS9407902
; GENERAL INFORMATION:
; APPLICANT: Street address: 4980 Carroll Canyon Road
; APPLICANT: City: San Diego
; APPLICANT: State/Province: California
; APPLICANT: Country: US
; APPLICANT: Postal code/Zip: 92121
; APPLICANT: Phone number: (619) 453-8030
; APPLICANT: Telex number:
; TITLE OF INVENTION: Materials and Methods for the Control of
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
```

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; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07902
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1180 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07902-28

Query Match      29.5%; Score 1153; DB 4; Length 1180;
Best Local Similarity 37.2%; Pred.No.6.4e-89;
Matches 282; Conservative 131; Mismatches 282; Indels 64; Gaps 25;

QY      5 NNNEVEIIDS--KNLSYPSNRNIDHSRYPTYNPNQPLQNTNYKEWLNMCQNTQYGDNP 62
Db      6 NKNEYETLNASQKLNISNN-----YRPIENSPKQLQSTNYKDWLNWCQQOQYGGDF 61
QY      63 ETPASADTTAAVSAAGTIVSGTLAGIGLTSISGPIGIIIGAIISFGTLITVFWPAGEQD 122
Db      62 ETPIDS---GELSAITVVGTLTGFGFTT---PLGL---ALIGFTLIPVLFPQAQDOS 111
QY      123 KTVMTQPIKNGEIVFDVTPLETESIKQLQTLQLEGFRQILOSYNTALDDWRKLKELQAPGLP 182
Db      112 NT-WSDFITQTKNIIKKEIASTYISNANKILNRSFNVIYHNHLKTWE-----NNPNPQ 165
QY      183 PSSALQQAALTLKIRFENVHNDIREIP--GFQLETYKTLILLPIYAQAANFHLNLQOQA 240
Db      166 NTQDVRTQIQLVHYHFQNVIPELVNSCPNPSDCDYNNILVSSYAQAANHLTVLNQAV 225
QY      241 ELADENADIHPSQIEPNAGTSDDYKLLKENIPKYSNYCANTYRGLNKLNEP-----295
Db      226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTKAIEDYTNVCVTTYKGLNLKTTDPSNLD 284
QY      296 -NMRWSIENDRYRMYTITVLDITIAQSFYDIKRYKDSIGRIGIKTELTRREIYTTINPD 354
Db      285 GNINWNTYRTKMTTAVLDLVALFPNYDVGKPI-----GVQSELTRREIYQV-LNFE 337
QY      355 RLTYLEIOPNLAIMBYNLTGRSLRFLSFLDELIFFTKNETYGNRLVGIANRNRSTYA---411
Db      338 ESPYKY--DFQYQEDSLTRP-HLFTWLDLSNFYEKAQTTNNPF-TSHYNMFHYTLDN 393
QY      412 TTGTEIIGERTGPPPTKTLIPESYKVSIVTDQVTPSPPNYIYFTINQIELYLNNSP 471
Db      394 ISQKSSVFGNNHVTDKLSL--GLATNIYIFLLNVISLDNKYLDNNYSKMDFFITNGT 451
QY      472 ---SNKLTYSAGNLNDKKTTFQFPVKDCKPIINPNCLPSYNSHILSQFSLFNY- 527
Db      452 RLLEKELT-AGSQIITYDVNKNIFGLPILKPRENQAIPFTFYDNYSHILSFIKSLSP 510
QY      528 -SYKIGLALNLYTGALGWTSHSSVNRNNAISDKIITMIPAIGNSLDTNSKVIEGFGHTG 586
Db      511 ATYK-----TQVYTF--WTHSSVDPKNTIYTHLTQIPAVKANSIGTASKKVQVGFHTG 563
QY      587 GNLVYLQSQGRLEICTRTNSTQSYIRLRYATNGAGNTLPNLSLTIPGVIGIPPORLNN 646
Db      564 GDLI--DPKDFKITCOHSNFQOQSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620
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QY 647 TSSGTYNNALQDGGYGFQFFSTVLP LNRPPIFNADV-SNSILIDKIEFPIITS 705
DB 621 TSSGDTYTNLKDFQYLEFSNEVKFAPNQISLVFNRSVYNTTTLIDKIEFLPIRS 680
QY 706 VQNEKQKLETIQPKINTFFTNHTKNTLNEATNYDID 744
DB 681 IREDEKQKLETVQOQIINTFFYANPKNTLQSELTDYDID 719

RESULT 3
US-09-224-024-31
; Sequence 31, Application US/09224024
; Patent No. 6056953
; GENERAL INFORMATION:
; APPLICANT: Leslie Hickie
; APPLICANT: Jewel Payne
; TITLE OF INVENTION: Materials and Methods for the Control of
; TITLE OF INVENTION: Calliphoridae Pests
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,024
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 686 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-224-024-31

Query Match 23.0%; Score 900; DB 2; Length 686;
Best Local Similarity 32.9%; Pred. No. 9.9e-68;
Matches 251; Conservative 115; Mismatches 268; Indels 128; Gaps 32

QY 5 NNNEYEIIIDSKNLSYPSNRNIDHSRYTYTNPNQPLQNTYKWLNNCGQNTQYGDNFET 64
DB 6 NNNEYEIFNAPSGFSKSN--YSRYPLANKPNQPLKNTNYKDLNVQDNQYGNAGN 63
QY 65 PASADTIAAVSAGTIVSGTLAGIGGTSISGPIGIGAILIISFGTILITVFWPAGEQDKT 124
DB 64 FVSSETIVGVSAGITVVGTMLG-----AFAAP--VLAAGIISFGTLLPIFW-QGSDPAN 114
QY 125 VNTQIKMGEIFVDTPPLE---SIKQLKLOTLEGFRQILOSYNTALDDWRKLRQLQAPGL 181
DB 115 VVQDLINLG----GRPIQIEDKNVINVLTSVTPIKNLDKYQEFFDKWEPAR----- 163
QY 182 PSSLAQQAALTILKIRFENVHN---DFIREIPGQLEYTKTLLPIYAQAANFHLNLLQO 238

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Qy		180	GUPPSALQQAALTUKIRFENVHNDFTREIPGFOLEYTKTLILLPIYAQAANFHNLQQ3	239
Dd	:	159	--NPGS--RALDVRNRNEFDLSLFTQYWPSPRVNTNFVFFLTVTYTAANLLHLRLDA	214
Qy	:	240	AELADEWNADTHPSQIEBNAGTSDDYKLLKENIPKYSNCANTYREGINKLRNEPNRW	299
Dd	:	215	SIFGEWGL-----STSTINNYNRQMKLTAEYSDHCVMYETGLAKUGSSAKOW	265
Qy	:	300	SIFENDYRRYMTITVLDTIAQFSFYDIKRYKDSIGRIGGIKTEITREIYTTFINFDRLTYL	359
Dd	:	266	IDYNQFRREMWTLVLDVVAFSNYDTRYPLA-----TTAQLTREVYT-----DPLGAV	314
Qy	:	360	ELOPNL-----AIMEYNLTRSGUR---LRSFLDELFTYKNETY-GNRLVIANGNNRST	409
Dd	:	315	DV-PNIGSWYDKAPSFSEIEKAARPPHFVDYITGLTVTYTKRSFTSDRYMYRWAGHOIS	373
Qy	:	410	YATTCITEIIYGBERTGPPTTKL----1PESYKY-SIVTDROVTPTSPPPNI-----	456
Dd	:	374	YKHIGTSTFTQMYG--TNQLQSTNSPDFNTYDIYKTLNSGAVLLDIDVPGVYTYTFOM	431
Qy	:	457	----YFTINOIELYLNNSPNSKLAYS-AGGNLSNDKKTDFQPFPVKDKCKPIINPNCLPS	511
Dd	:	432	PETEFEWMNQ-----NNTRKTLAYKPASKDOI DRTEDSELELPPTSQO-----PN	478
Qy	:	512	YNSYSHILSQSFLFNYSYKIGIALNILYTGALGWTHSSHVNRNAISDKIITMIPA KGSN	571
Dd	:	479	YESYSHRHLGHIT-FIYS-----SSTSTYVPVFWSHTRSADLTNTVASGEITQIPGKSST	532
Qy	:	572	LDTNSKVLEGCHGTGNLA VLOSQ-GRLEITCRTPNSTOSYIYRLAYATNGAGNTL PNIS	630
Dd	:	533	ICGRNTYI IKGRTYGDDVALUTDRIGSCFQMIPPES-QRFRIIRIYASNETS-----Y	585
Qy	:	631	LTIPVGIGIPQORLNPFTSGNTYNNLOYGPGYFQFPSTVTLPLNRIPIFNRA DVSNS	690
Dd	:	586	ISLYGLANSOTLKFNQYTSKNENDLIYNDEKFIEYPRVISVNASSNIQRSLSIGITWTN	645
Qy	:	691	ILIIDIKBIFPITSSVRONREKQKLETIO TKINTFFTNNHTKNTLNTIATNYDID	744
Dd	:	646	LFPILOIRISFIPDETYYEATED---LEAAKAVNALFTN-TKOGLOGPVTDYEVN	695

## RESULT 6

US-08-315-468-6  
Sequence 6, Application US/08315468  
Patent No. 5554534  
GENERAL INFORMATION:  
APPLICANT: Michaels, Tracy Ellis  
APPLICANT: Fonceerrada, Luis  
APPLICANT: Narva, Kenneth E.  
TITLE OF INVENTION: Process for Controlling Scarab Pests  
TITLE OF INVENTION: with Bacillus thuringiensis Isolates  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/315,468  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/014,941  
FILING DATE: 01 FEB 1993  
APPLICATION NUMBER: 07/828,430  
FILING DATE: 30-JAN-1992

QY 569 GNSLDTNSKVIIEGPGHTGNLVYLO-----SQGRLEITCRTPNSTQSYIIRLRYATNGAGN 624  
Db 520 AYALSSGASIIIEGPGFTGGNLLFLKSSNSIAKPKVTLSAALLQRYRVRIRYAST-----575  
QY 625 TLENISLTIPGVGIGPPQRLNNTFSGTNNVNLQY--GDFGY--FQPPSTVTLPLNRNIPF 680  
Db 576 --TNLRFLV-----QNSNDFLVIYINKTNWIDGDLTYQTFDFATS-----NSNMGF 620  
QY 681 IFNRAD-----VNSNLIIDKIEFIPI 702  
Db 621 SGTNDNFIIGAESFVSNKIIYIDKIEFIPV 650

## RESULT 7

US-07-941-650A-4  
; Sequence 4, Application US/07941650A  
; Patent No. 6294184  
; GENERAL INFORMATION:  
; APPLICANT: Uveda, Kendrick A.  
; APPLICANT: Bradfisch, Gregory A.  
; TITLE OF INVENTION: Process for Controlling Lepidopteran Pests  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/941,650A  
; FILING DATE: 19920908  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/758,020  
; FILING DATE: 12-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/658,935  
; FILING DATE: 21-FEB-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/642,112  
; FILING DATE: 16-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 651 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: YES  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; STRAIN: tolworthi  
; INDIVIDUAL ISOLATE: 43f  
; IMMEDIATE SOURCE:  
; CLONE: E. coli XL1-Blue (pML98-4), NRRL B-18291  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..651  
; US-07-941-650A-4

Query Match 18.2%; Score 710; DB 2; Length 651;  
Best Local Similarity 28.9%; Pred. No. 1.4e-51;  
Matches 217; Conservativity 115; Mismatches 270; Indels 148; Gaps 31;  
QY 1 MNQNNNEYEIID-SKNLSYSPSNRNIDHSRYVYTNPNQPLQNTYKKEWLMCOGNTQYG 59  
Db 1 MNPNNRSEYDTIKVTPNSLPN-----HNQYPLADNPNSTLEELNYKEFLRMTADNST-- 54  
QY 60 DNFETPASADTTAAVSAGTIVSGTLLAGIGGTSISGPIIGAIISFGTLLTVFWPAG 119  
Db 55 ---EVLDSSTVADAVGTGIVSVVQILGVVG-----VPFAGALTSFYQSFLNAIWPS- 102  
QY 120 EODKTVWTFQIKMGIFVDVTPLTSTESIKQLQTLLEGFRQILQSYNTALDDWRKLKELQAP 179  
Db 103 --DADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDVYNALOSWK----- 153  
QY 180 GLPPSSALQQAALTUKIRPENVNDFIRIPQFQLETYKTKLLPIYAQAANFHLNLLQOG 239  
Db 154 -APVNLRSRSDRIRLELSQAESHFRNSMPFVSKFEVLFLPTTYAQAANTHLLLLKDA 212  
QY 240 AELADEWNADIHPSQIEPNAGTSD--YYKLLKENIPKSYNCANTYREGLNKLNENPN 296  
Db 213 QVFGGEWGY-----SSEDAIEFYQRLKLTQYTDHCNVNWNVGLNSLRGTY 260  
QY 297 MEWSIFNDYRYMTITVLDTIAQPSFYDIKRYKDSIGRIGGKTELTRYITTEINFDR 356  
Db 261 DAWKFNRRREMTLTVLDLIVLFPFVRLVSK-----GVKTELTRDIFDPI-FTLN 313  
QY 357 TYLEIQPNLAIMEYNLTRSGLRFLSFLDELIFYTK-----NETYGNRLVGIANR 405  
Db 314 ALQEVGPTFESSIENSIRKP--HLFDYLRGIEFHTLRPGVSGKDSFNYSNGY---VETR 368  
QY 406 NRSTYATTCETIIGERTGPTTKLIPESKVSIVTRQV--TETSFPN--IYFTIN 461  
Db 369 PSIGSNDTITSPFYGDKSIEPIQK--LSPDGQKV---RTIANTDIAAAPPDCKIYFGVT 422  
QY 462 QIELYLNPSNKL--TYSA-----GGNLSNDK---KTTFQFPVKKCKPPIINPNC 508  
Db 423 KVDFSGYDDQKNETSTQYDSKRYNGYLGQAQSIDQLPETTD--EPLSK----- 470  
QY 509 LPSYNSYSHLSQFSLFNYSYKIGLALNLYTGALGWTSHSSVNRNNAISDKIITMIPA 568  
Db 471 -----AYSHQLNVAECFLMQDRRTI--PFFT---WTHRSVDFTNTIDAEKITQLPVVK 519  
QY 569 GNSLDTNSKVIIEGPGHTGNLVYLO-----SQGRLEITCRTPNSTQSYIIRLRYATNGAGN 624  
Db 520 AYALSSGASIIIEGPGFTGGNLLFLKSSNSIAKPKVTLSAALLQRYRVRIRYAST----- 575  
QY 625 TLENISLTIPGVGIGPPQRLNNTFSGTNNVNLQY--GDFGY--FQPPSTVTLPLNRNIPF 680  
Db 576 --TNLRFLV-----QNSNDFLVIYINKTNWIDGDLTYQTFDFATS-----NSNMGF 620  
QY 681 IFNRAD-----VNSNLIIDKIEFIPI 702  
Db 621 SGTNDNFIIGAESFVSNKIIYIDKIEFIPV 650

## RESULT 8

US-08-996-441B-112  
; Sequence 112, Application US/08996441B  
; Patent No. 6023013  
; GENERAL INFORMATION:  
; APPLICANT: English, Leigh H.  
; APPLICANT: Brussock, Susan M.  
; APPLICANT: Malvar, Thomas M.  
; APPLICANT: Bryson, James W.  
; APPLICANT: Kulesza, Caroline A.  
; APPLICANT: Walters, Frederick S.  
; APPLICANT: Slatin, Stephen L.  
; APPLICANT: Von Terssch, Michael A.  
; APPLICANT: Romano, Charles  
; TITLE OF INVENTION: INSECT-RESISTANT TRANSGENIC PLANTS



Qy 60 DNFETASADTIAAVSAGTIVSGTLLAGIGGLTSISGPIGIIGAIISFGTLITVFWPAG 119

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Db 63 ---EVLDSSTVKDVGTSVWGQILGWG-----VPPAGALTSFYQSPLNALWPS- 110
Qy 120 EQDXTVWTQIKMGEIFVDTPLTESIKQLKLTLEGFROILOSINTALDDWRKLKQLAP 179
Db 111 --DADPWKAFMAQVEILIDKIEYAKSKALAELOQLNNFEDYVVALDSWK----- 161
Qy 180 GLPPSALQQAALTUKIRFENVHDFIREIPGFOLEYTKTLPIYAQAANFHLNLQOG 239
Db 162 -APVNLRSRQDRIRLEFSQAESHFNMPSPFAVKFVLFTPYAQAANTHLLLLKOA 220
Qy 240 AELADEWADIHPSQIEPNAGTSD--YYKLKENIPKYSNYCANTYREGNKLKRNEN 296
Db 221 QVFGGEWGY-----SSEDIAEFYQQLKLTQQYTDHCYVNVVGLNSLGSY 268
Qy 297 MRWSIFNDYRRYMTITVLDITIAQFSYDIKRYKDSIGRIGGKTELTRIYITEINFDRL 356
Db 269 DAWVKFNFRREMTLTVDLIVLPPFYDVRLYSK-----GVKTELTRDIFTDPI-FTLN 321
Qy 357 TYLEIOPNLAIMYENLRSGLRFLSFLDELIFYTK-----NETYGNRLVGIANR 405
Db 322 ALQEGYPTFSSSIENSIRKP--HLFDYLRGIEFHTLRPGYSGKDSFNWWSGNY---VETR 376
Qy 406 NRSTYATTGTETIYIGERTGPPTTKTILIPFESYKVSIVTDQV--TPTSPPN--IYFTIN 461
Db 377 PSIGSNDTITSPFYGDKSIEPIQK--LSPDGQKVY---RTIANTDIAAFPDKGIYFVGT 430
Qy 462 QIELYLNNSPKL---TYSA-----GGNLSNDK---KTDFQFPVKCKCKPIINPNC 508
Db 431 KVDFSQYDDQKNETSTQTYDSKRYNGYLGAQDSIDLPPETTD--EPLEK----- 478
Qy 509 LPSYNSYSHLSQFSLFNYSYKIGLALNLTLYTGALGTHSSVNRNNAISDKIITMIPAK 568
Db 479 -----AYSHQLNABCFMLQDRGTI--PFFT-----WTHRSVDFFTIDAEEKITQLPVVK 527
Qy 569 GNSLDTNSKVIIEGPGHTGGNVLVYQ-----SQGRLEITCTPNSTQSYIRLRYATNGAGN 624
Db 528 AYALSSGASIIIEGPGFTGGNLLFLKSSNSIAKFKVTLNSAALLQRYVRIRYAST---- 593
Qy 625 TLPNISLTIPGVIGIPQRLNNTFSGTNNYLNQY--GDFGY--FQFPSTVTLPLNRNIPF 680
Db 584 --TNLRLFV-----QNSNNDFLVIYINKTNIDGLTYQTFDFATS-----NSNMGF 628

RESULT 10
US-08-993-170A-112
; Sequence 112, Application US/08993170A
; Patent No. 6063597
; GENERAL INFORMATION:
; APPLICANT: English, Leigh H.
; APPLICANT: Bruesock, Susan M.
; APPLICANT: Malvar, Thomas W.
; APPLICANT: Bryson, James W.
; APPLICANT: Kulesza, Caroline A.
; APPLICANT: Walters, Frederick S.
; APPLICANT: Slatin, Stephen L.
; APPLICANT: Von Tersch, Michael A.
; TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,170A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-170A-112

Query Match 18.2%; Score 710; DB 2; Length 659;
Best Local Similarity 28.9%; Pred. No. 1.5e-51;
Matches 217; Conservative 115; Mismatches 270; Indels 148; Gaps 31;

Qy 1 MNQNNNEVEID-SKNLSYSPSNRNIHDSRYPTYNPQLONTNYKEWLNCOGNTQYG 59
Db 9 MNPNNRSEYDTTKVPSNSELPTN----HNQYPLADNPSTLBELNYKEFLRTADNST-- 62
Qy 60 DNFETPASADTTAAVSAGTIIVSGTLLAGIGGLTISGPIIGIICAIISFGTILITVWPAG 119
Db 63 ---EVLDSSTVKDVGTSVWGQILGWG-----VPPAGALTSFYQSPLNALWPS- 110
Qy 120 EQDXTVWTQIKMGEIFVDTPLTESIKQLKLTLEGFROILOSINTALDDWRKLKQLAP 179
Db 111 --DADPWKAFMAQVEILIDKIEYAKSKALAELOQLNNFEDYVVALDSWK----- 161
Qy 180 GLPPSALQQAALTUKIRFENVHDFIREIPGFOLEYTKTLPIYAQAANFHLNLQOG 239
Db 162 -APVNLRSRQDRIRLEFSQAESHFNMPSPFAVKFVLFTPYAQAANTHLLLLKOA 220
Qy 240 AELADEWADIHPSQIEPNAGTSD--YYKLKENIPKYSNYCANTYREGNKLKRNEN 296
Db 221 QVFGGEWGY-----SSEDIAEFYQQLKLTQQYTDHCYVNVVGLNSLGSY 268
Qy 297 MRWSIFNDYRRYMTITVLDITIAQFSYDIKRYKDSIGRIGGKTELTRIYITEINFDRL 356
Db 269 DAWVKFNFRREMTLTVDLIVLPPFYDVRLYSK-----GVKTELTRDIFTDPI-FTLN 321
Qy 357 TYLEIOPNLAIMYENLRSGLRFLSFLDELIFYTK-----NETYGNRLVGIANR 405
Db 322 ALQEGYPTFSSSIENSIRKP--HLFDYLRGIEFHTLRPGYSGKDSFNWWSGNY---VETR 376
Qy 406 NRSTYATTGTETIYIGERTGPPTTKTILIPFESYKVSIVTDQV--TPTSPPN--IYFTIN 461
Db 377 PSIGSNDTITSPFYGDKSIEPIQK--LSPDGQKVY---RTIANTDIAAFPDKGIYFVGT 430
Qy 462 QIELYLNNSPKL---TYSA-----GGNLSNDK---KTDFQFPVKCKCKPIINPNC 508
Db 431 KVDFSQYDDQKNETSTQTYDSKRYNGYLGAQDSIDLPPETTD--EPLEK----- 478
Qy 509 LPSYNSYSHLSQFSLFNYSYKIGLALNLTLYTGALGTHSSVNRNNAISDKIITMIPAK 568
Db 479 -----AYSHQLNABCFMLQDRGTI--PFFT-----WTHRSVDFFTIDAEEKITQLPVVK 527
Qy 569 GNSLDTNSKVIIEGPGHTGGNVLVYQ-----SQGRLEITCTPNSTQSYIRLRYATNGAGN 624
Db 528 AYALSSGASIIIEGPGFTGGNLLFLKSSNSIAKFKVTLNSAALLQRYVRIRYAST---- 593
Qy 625 TLPNISLTIPGVIGIPQRLNNTFSGTNNYLNQY--GDFGY--FQFPSTVTLPLNRNIPF 680
Db 584 --TNLRLFV-----QNSNNDFLVIYINKTNIDGLTYQTFDFATS-----NSNMGF 628
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QY 681 IFNRAD-----VNSILIIDKIEPIPI 702  
 Db 629 SGTNDFTIIGAESFVSNEKIYIDKIEPIPV 658

## RESULT 11

US-08-993-775B-112  
 ; Sequence 112, Application US/08993775B  
 ; Patent No. 6077824  
 ; GENERAL INFORMATION:  
 ; APPLICANT: English, Leigh H.  
 ; APPLICANT: Brussock, Susan M.  
 ; APPLICANT: Malvar, Thomas M.  
 ; APPLICANT: Bryson, James W.  
 ; APPLICANT: Kulesza, Caroline A.  
 ; APPLICANT: Walters, Frederick S.  
 ; APPLICANT: Slatin, Stephen L.  
 ; APPLICANT: Von Tersch, Michael A.  
 ; TITLE OF INVENTION: METHODS FOR IMPROVING THE ACTIVITY OF  
 ; TITLE OF INVENTION: DELTA-ENDOTOXINS AGAINST INSECT PESTS  
 ; NUMBER OF SEQUENCES: 113  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P.O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: USA  
 ; ZIP: 77210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/993,775B  
 ; FILING DATE: 18-DEC-1997  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kitchell, Barbara S.  
 ; REGISTRATION NUMBER: 33,928  
 ; REFERENCE/DOCKET NUMBER: MECO:150  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 512/418-3000  
 ; TELEFAX: 512/474-7577  
 ; INFORMATION FOR SEQ ID NO: 112:  
 ; SEQUENCE CHARACTERISTICS:  
 ; TYPE: amino acid  
 ; LENGTH: 659 amino acids  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; US-08-993-775B-112

Query Match 18.2%; Score 710; DB 2; Length 659;  
 Best Local Similarity 28.9%; Pred. No. 1.5e-51;  
 Matches 217; Conservative 115; Mismatches 270; Indels 148; Gaps 31;  
 QY 1 MNQNNNEYETID-SKNLSYSPNRNIDHSRYPTNNPQLONTNYKEWLNMCQNTQYG 59  
 Db 9 MNPNRSEYDIKVTNPSELPTN-----HNQYPLADNPSTLEELNYKEFLRKTADNST-- 62  
 QY 60 DNFTFASADTAAVSAGTIYSGTLLAGIGLTSISGPIGIIAISFGTLITVFWPAG 119  
 Db 63 ---EVLDSSTVKDAVGTGSGVVGILGVG-----VPPAGALTSPYQSFLNAWFS- 110  
 QY 120 EQDKVTWTFQTKMEIIFVDTPLTESIKQLKQTLQLEGFRQILQSNVNTALDDWRKLRLOAP 179  
 Db 111 --DADPKFAFWAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALDSWKK----- 161  
 QY 180 GLPSSALQQAALTILKIRFENVHDFIREIPGQLETYKTLILLPIYQAANFHLNLLQOG 239  
 Db 162 -APVNLRRSQDRIRLELFSQAESHFRNMPSPFAVSFEVLFPLPYAQAANTHLLLLKDA 220

QY 240 AELADEWNADIHPSQIEPNAGTSD-----YKLLKENIPKYSNYCANTYREGLNKLRNEPN 296  
 Db 221 QVGEEMGY-----SSEDIAEAFQRLKLTQQYTDHCVNWNVGLNSLRGSTY 268  
 QY 297 MRNSIENDYRYMTITVLDIAQFSFYDIKRYKDSIGRIGIKTELTRREIYTTINFDRL 356  
 Db 269 DAWVKFRFRREMTLTVDLILVLPFYDVRYSK-----GVKTELTRDIFTDPI-FTLN 321  
 QY 357 TYLEIQPNLAIMEYNLTRSGRLRFSFLDELIFVTK-----NETYGNRLVGIANR 405  
 Db 322 ALQEVGPTFSSIENSIRKP--HLFDYLRGIEFHTRLRPGYSGKDSFNWMSGY---VETR 376  
 QY 406 NRSTYATGTIELIYGERTGPTTKTLIPFESYKSVIVTDROV--TPTSPPPN--IYFTIN 461  
 Db 377 PSIGSNDTITSPFYGDKSIEPIQK--LSFDGQKY---RTIANTDIAAEPDGKIYFGVT 430  
 QY 462 QIELYLNNSPSNKL---TYSA-----GGNLSNDK---KTTDFQFPVKDKCKPIINPNC 508  
 Db 431 KVDFSQYDDQKNETSTQTYDSKRYNGYLGAQDSIDQLPETTD--EPEK----- 478  
 QY 509 LPSYNSYSHILSQFSLFNYSYKIGLALNLYTGALGWTSHSVNRRNAISDKIITMIPA 568  
 Db 479 -----AYSHQLNVAECFLMQDRRCTI--PPFT-----WTHRSVDFENIDAETIQLPVK 527  
 QY 569 GNSLDTNSKVIIEGPGHTGGLVYLQ-----SQRLIEITCRTPNSTQSYVIRURYATNGAGN 624  
 Db 528 AYALSSGASITIEGPGFTGCGNLLFLKSSNSITAKFKVTLNSAALLQRYRVRIRYAST----- 583  
 QY 625 TLPNISITIFGVIGIPQRLNNTFSGTNNYLNQY--GDFGY--QFPSTVTLPLNRNIPP 680  
 Db 584 --TNLRUFV-----QNSNDFLVIYINKTNMIDGLTYQTDFATS-----NSNMGF 628  
 QY 681 IFNRAD-----VNSILIIDKIEPIPI 702  
 Db 629 SGTNDFTIIGAESFVSNEKIYIDKIEPIPV 658

## RESULT 12

US-09-427-770-112  
 ; Sequence 112, Application US/09427770  
 ; Patent No. 6620988  
 ; GENERAL INFORMATION:  
 ; APPLICANT: English, Leigh H.  
 ; APPLICANT: Brussock, Susan M.  
 ; APPLICANT: Malvar, Thomas M.  
 ; APPLICANT: Bryson, James W.  
 ; APPLICANT: Kulesza, Caroline A.  
 ; APPLICANT: Walters, Frederick S.  
 ; APPLICANT: Slatin, Stephen L.  
 ; APPLICANT: Von Tersch, Michael A.  
 ; APPLICANT: Romano, Charles  
 ; TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED  
 ; TITLE OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS  
 ; NUMBER OF SEQUENCES: 113  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P.O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: USA  
 ; ZIP: 77210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/427,770  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/993,722  
 ; FILING DATE: 18-DEC-1997





APPLICANT: Bryson, James W.  
APPLICANT: Kulesza, Caroline A.  
APPLICANT: Walters, Frederick S.  
APPLICANT: Slatin, Stephen L.  
APPLICANT: Von Terssch, Michael A.  
APPLICANT: Romano, Charles  
TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED  
TITLE OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/993, 722A  
FILING DATE: 18-DEC-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: MECO:149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3106  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 652 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-993-722A-110

Query Match 18.0%; Score 704; DB 2; Length 652;  
Best Local Similarity 29.0%; Pred. No. 4.7e-51;  
Matches 217; Conservative 116; Mismatches 272; Indels 142; Gaps 32;  
Qy 1 MNQNNNEYEIID-SKNLSYPSNRNIDHSYVYNNPNQPLQNTNKEWLNMCQ-GNTQY 58  
Db 1 MNPNNRSEHDTIKVTPNSELPTN-----HNQYPLADNPNTLEELNYKEFLRMTEDSSTEV 56  
Qy 59 GDNFETPASADTIA-AVSAGTIVSGTLGAGIGGLTSISGPIGIGAIISFGTLITVFWP 117  
Db 57 LDN-----STVKDAVGTGIVGVGILGVVG-----VPFAGALTSFYQSPLDTIMP 101  
Qy 118 AGSQDKTVTQFIMGGEIFVDVTPLETESIKOLKLTLEGFRQILQSNVTALDDWRKLRQ 177  
Db 102 S---DADPWAFMAQVEVLIDKIEYAKSKALAEQLQGNFEDYVNALNSWK----- 153  
Qy 178 APGLPPSALQQAAALTLLKIRFENVHNDPIREIPGQLETYKTLPIYQAANFHLNLQ 237  
Db 154 ---TPLSLRSRQSDRELPSQAEHSFRNMPSPFAVSKFEVLPLPYQAANTHLLLLK 210  
Qy 238 QGAELADENMADIPHSQIEBNAGTSDDYKLLKENIPKYSNCANTYREGINKLRNEPNM 297  
Db 211 DAQVFGEEGYS-----SEDAEFYHRQLKLT-QQYTDHCVMYVGLNGLRGSTDYD 261  
Qy 298 RWSIFNDYRRYMYITVLDTTAQSPFYDIKRYKDSIGRIGIKTELREIYTTTINFDRLT 357  
Db 262 AWVKFNFRREMTLVLDLIVLPFPYDRLYSK-----GVKTELTRDIFDPI-PSLNT 314  
Qy 358 YLEIQPNLATMEYNLTRSGLRSLRFLDELIFYTK-----NETYGNRLVGIANRN 406  
Db 315 LOEYGPFTFLSIENSIRP--HLFDYLOGIEFHLRQGYSGKDSFNWGSNY---VETRP 369  
Qy 407 RSTVATTGTBIYIGRTGPTTKTLIPFESYKYSIVTDQV--TPTSFPFN--IYFTINQ 462

Db 370 SIGSSKTIITSPFYGDKSTEPVOK--LSPDGQKVY-----RTIANTDVAAMPNGKIYFGVTK 423  
Qy 463 IELYLNNSPSNKL-----TYSA-----GGNLNDK---KTTDFQFPVKQCKRPIINPCL 509  
Db 424 VDFSQYDDQKNETSTQTYDSKRNNGHVGAQDSIDQLPPETTD--EPLK----- 470  
Qy 510 PSVNSYSHILSQSLFNFYSYKIGLALNILYTGALGWTSHSSVNRNNAISDKIITMIPAIG 569  
Db 471 ----AYSHQLNYABCFELMODRGTI--PFPT-----WTHRSVDFFTIDAETIQLPVPVKA 520  
Qy 570 NSLDTNSKVIIEGPGHTGGLVYLQ-----SQGRLEITCRTPNSTQSYIIRLYATNGAGNT 625  
Db 521 YALSSGASIIIEGPGTGGNLLFLKSSNSIAKFVKTLSAALLQRYVRIRVAST----- 575  
Qy 626 LPNISLITPGVIGIPPORLNTFSGTNYNNLQY--GDFGYFQFPSPSTVTLPLNRNIPF--- 680  
Db 576 -TNLRLFV-----QNSNNDFIYIYINKTNIDDDLTQTDFDLATT---NSNMGFSGD 623  
Qy 681 -----IFNRADVSNSTILIIDKIEFPI 702  
Db 624 TNELIIGAESFVSNEKIYIDKIEFIPV 650

Search completed: December 15, 2005, 10:56:39  
Job time : 50 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2005, 10:47:44 ; Search time 168 Seconds  
(without alignments)  
1850.387 Million cell updates/sec

Title: US-10-782-570-2

Perfect score: 3906

Sequence: 1 MNQNNNEIIDSKNLSYP.....FFTNHTKTLNIBATNYDID 744

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3906	100.0	744	4	US-10-782-570-2
2	3623	92.8	694	4	US-10-782-570-4
3	3318	84.9	735	5	US-10-783-417-2
4	1158	29.6	1180	4	US-10-782-141-12
5	1158	29.6	1180	4	US-10-782-096-14
6	1158	29.6	1180	4	US-10-782-570-10
7	1158	29.6	1180	5	US-10-783-417-8
8	1158	29.6	1180	5	US-10-781-979-14
9	901	23.1	1109	3	US-09-756-526A-4
10	901	23.1	1109	4	US-10-345-020-4
11	897	23.0	1109	4	US-10-342-821-4
12	897	23.0	675	4	US-10-782-141-17
13	897	23.0	675	4	US-10-782-096-18
14	897	23.0	675	4	US-10-782-570-14
15	897	23.0	675	5	US-10-783-417-12
16	897	23.0	675	5	US-10-781-979-19
17	897	23.0	675	5	US-10-926-819-16
18	819	21.0	1136	4	US-10-782-141-13
19	819	21.0	1136	5	US-10-781-979-15
20	819	21.0	1136	5	US-10-929-754-1
21	720	18.4	1210	4	US-10-032-717-4
22	720	18.4	1210	4	US-10-414-637-4
23	720	18.4	1210	4	US-10-606-320-4
24	720	18.4	1210	4	US-10-746-914-4
25	712.5	18.2	780	6	US-11-018-615-29
26	712.5	18.2	1169	6	US-11-018-615-25
27	710	18.2	659	4	US-10-614-076-112

28	710	18.2	659	4	US-10-782-096-12	Sequence 12, Appl
29	710	18.2	659	4	US-10-782-570-9	Sequence 9, Appl
30	710	18.2	659	5	US-10-783-417-7	Sequence 7, Appl
31	709.5	18.2	682	4	US-10-782-096-20	Sequence 20, Appl
32	709.5	18.2	682	4	US-10-782-570-16	Sequence 16, Appl
33	709.5	18.2	682	5	US-10-783-417-14	Sequence 14, Appl
34	709.5	18.2	682	5	US-10-781-979-21	Sequence 21, Appl
35	704	18.0	652	4	US-10-232-665-4	Sequence 4, Appl
36	704	18.0	652	4	US-10-614-076-110	Sequence 110, App
37	703	18.0	1206	4	US-10-032-717-2	Sequence 2, Appl
38	703	18.0	1206	4	US-10-414-637-2	Sequence 2, Appl
39	703	18.0	1206	4	US-10-606-320-2	Sequence 2, Appl
40	703	18.0	1206	4	US-10-746-314-2	Sequence 2, Appl
41	697	17.8	652	4	US-10-232-665-6	Sequence 6, Appl
42	695	17.8	652	4	US-10-232-665-2	Sequence 2, Appl
43	695	17.8	652	4	US-10-614-076-4	Sequence 4, Appl
44	695	17.8	652	4	US-10-614-076-10	Sequence 10, Appl
45	695	17.8	652	4	US-10-614-076-28	Sequence 28, Appl

## ALIGNMENTS

### RESULT 1

US-10-782-570-2

; Sequence 2, Application US/10782570

; Publication No. US20040210965A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Koziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and

; FILE REFERENCE: 045600/274144

; CURRENT APPLICATION NUMBER: US/10782,570

; CURRENT FILING DATE: 2004-02-19

; PRIOR APPLICATION NUMBER: 60/448,812

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 744

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-782-570-2

Query Match 100.0%; Score 3906; DB 4; Length 744;

Best Local Similarity 100.0%; Pred. No. 4.2e-294;

Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNQNNNEIIDSKNLSYPNNDHSRYPYNNPNQPLONTNYKEWLNCCOQNTQGD 60

Db 1 MNQNNNEIIDSKNLSYPNNDHSRYPYNNPNQPLONTNYKEWLNCCOQNTQGD 60

Qy 61 NFETFASADTAAVSAGTIVSGTLLAGIGGTSISGPIIGAIISFGTLITVFWPAGE 120

Db 61 NFETFASADTAAVSAGTIVSGTLLAGIGGTSISGPIIGAIISFGTLITVFWPAGE 120

Qy 121 QDKTVTQTFKMGIFVDDTPTLITESIKQLQTLSEGFQILQSYNTALDDWKLRLQAPG 180

Db 121 QDKTVTQTFKMGIFVDDTPTLITESIKQLQTLSEGFQILQSYNTALDDWKLRLQAPG 180

Qy 181 LPPSSALQQALTLKIRFENVHNDPIREIFQFQLETYKTLPIYQAANPHNLQOGA 240

Db 181 LPPSSALQQALTLKIRFENVHNDPIREIFQFQLETYKTLPIYQAANPHNLQOGA 240

Qy 241 ELADENWADIHPSQIEPNAGTDDYYKLLKENIPKYSNYCANTYREGINKLRNPNMWS 300

Db 241 ELADENWADIHPSQIEPNAGTDDYYKLLKENIPKYSNYCANTYREGINKLRNPNMWS 300

Qy 301 IFNDYRRYMTITVLDITTAQFSFYDIKRYKDSIGRIGGIKTBLTREIYTTINFDRLTYLE 360

Db 301 IFNDYRRYMTITVLDTIAQSFVDIKRYKDSIGRIGGKTELREIYTTIEFDRLTYLE 360  
Qy 361 IQPNLAIMEYNLRSGRLRFSFLDELIFPYTKNETYGNRLVGIANRNRSTVATTGTEIIYG 420  
Db 361 IQPNLAIMEYNLRSGRLRFSFLDELIFPYTKNETYGNRLVGIANRNRSTVATTGTEIIYG 420  
Qy 421 ERTGPPPTTKLIPPEYSKYVSIIVTDROVTPTSPPPNIYFTINOJELLYNNSPSNKLTVSAG 480  
Db 421 ERTGPPPTTKLIPPEYSKYVSIIVTDROVTPTSPPPNIYFTINOJELLYNNSPSNKLTVSAG 480  
Qy 481 GNLNDKKTTFDQFPVVKCKPPIINPNCPLPSYNSYSHILSQSFLFNYSYKIGLALNLYT 540  
Db 481 GNLNDKKTTFDQFPVVKCKPPIINPNCPLPSYNSYSHILSQSFLFNYSYKIGLALNLYT 540  
Qy 541 GALGWTSSVNRNNAISDKIITWIPAIKGNSLDTNSKVIIEGPGHTGGLVYLOSQRLEI 600  
Db 541 GALGWTSSVNRNNAISDKIITWIPAIKGNSLDTNSKVIIEGPGHTGGLVYLOSQRLEI 600  
Qy 601 TCRTPNSTQSYIRLRVATNGAGNTLPNISLTIPGVIGIPPORLNNTFSGTNNLYQYGD 660  
Db 601 TCRTPNSTQSYIRLRVATNGAGNTLPNISLTIPGVIGIPPORLNNTFSGTNNLYQYGD 660  
Qy 661 FGYPQFPSTVTLPLNRNIPFINRADVSNLSIILDKIEFIPITSSVRQNRKOKLETIQ 720  
Db 661 FGYPQFPSTVTLPLNRNIPFINRADVSNLSIILDKIEFIPITSSVRQNRKOKLETIQ 720  
Qy 721 KINTFTNHTKNTLNIEATNYDID 744  
Db 721 KINTFTNHTKNTLNIEATNYDID 744

RESULT 2  
US-10-782-570-4  
; Sequence 4, Application US/10782570  
; Publication NO. US20040210965A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and  
; FILE REFERENCE: 045600/274146  
; CURRENT APPLICATION NUMBER: US/10/782,570  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 694  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-570-4

Query Match 92.8%; Score 3623; DB 4; Length 694;  
Best Local Similarity 100.0%; Pred. No. 3.6e-272;  
Matches 694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 51 MCQNTQYGNFETFASADTIAAVSAGTIYVSGTLLAGIGLTSISGPIGIIIGAIISFGT 110  
Db 1 MCQNTQYGNFETFASADTIAAVSAGTIYVSGTLLAGIGLTSISGPIGIIIGAIISFGT 60  
Qy 111 LITVFWPAGBQDKVTWTFQIKMGEIFVDTPLTSLIKQLKLTLEGFRQILQSYNTALDDW 170  
Db 61 LITVFWPAGBQDKVTWTFQIKMGEIFVDTPLTSLIKQLKLTLEGFRQILQSYNTALDDW 120  
Qy 171 RKLRLQAPGLPSSALQQAALTLKIRFENVHNDFREIPGQFLETYKTLILLPIYQAAN 230  
Db 121 RKLRLQAPGLPSSALQQAALTLKIRFENVHNDFREIPGQFLETYKTLILLPIYQAAN 180

Qy 231 FHLNLQQAELADEWNADIHPSQIEPNAGTSDDDYVYKLLKENIPKYSNYCANTYREGLNK 290  
Db 181 FHLNLQQAELADEWNADIHPSQIEPNAGTSDDDYVYKLLKENIPKYSNYCANTYREGLNK 240  
Qy 291 LRNEPNMRWSIFNDYRRYMTITVLDTIAQSFVDIKRYKDSIGRIGGKTELREIYTTIE 350  
Db 241 LRNEPNMRWSIFNDYRRYMTITVLDTIAQSFVDIKRYKDSIGRIGGKTELREIYTTIE 300  
Qy 351 INFDRLTYLEIQPNLAIMEYNLRSGRLRFSFLDELIFPYTKNETYGNRLVGIANRNRSTY 410  
Db 301 INFDRLTYLEIQPNLAIMEYNLRSGRLRFSFLDELIFPYTKNETYGNRLVGIANRNRSTY 360  
Qy 411 ATTGTETIYIGERTGPPPTTKLIPPEYSKYVSIIVTDROVTPTSPPPNIYFTINOJELLYNNS 470  
Db 361 ATTGTETIYIGERTGPPPTTKLIPPEYSKYVSIIVTDROVTPTSPPPNIYFTINOJELLYNNS 420  
Qy 471 PSNKLTYSAGGNLSNDKKTTFDQFPVVKCKPPIINPNCPLPSYNSYSHILSQSFLFNYSYK 530  
Db 421 PSNKLTYSAGGNLSNDKKTTFDQFPVVKCKPPIINPNCPLPSYNSYSHILSQSFLFNYSYK 480  
Qy 531 IGLALNLYTGALGWTSSVNRNNAISDKIITWIPAIKGNSLDTNSKVIIEGPGHTGGLV 590  
Db 481 IGLALNLYTGALGWTSSVNRNNAISDKIITWIPAIKGNSLDTNSKVIIEGPGHTGGLV 540  
Qy 591 YLQSQGRLEITCRTPNSTQSYIRLRVATNGAGNTLPNISLTIPGVIGIPPORLNNTFSG 650  
Db 541 YLQSQGRLEITCRTPNSTQSYIRLRVATNGAGNTLPNISLTIPGVIGIPPORLNNTFSG 600  
Qy 651 TYNNLQYGDGFGYFQFPSTVTLPLNRNIPFINRADVSNLSIILDKIEFIPITSSVRQNR 710  
Db 601 TYNNLQYGDGFGYFQFPSTVTLPLNRNIPFINRADVSNLSIILDKIEFIPITSSVRQNR 660  
Qy 711 EKQKLETIQTKINTFTNHTKNTLNIEATNYDID 744  
Db 661 EKQKLETIQTKINTFTNHTKNTLNIEATNYDID 694

RESULT 3  
US-10-783-417-2  
; Sequence 2, Application US/10783417  
; Publication NO. US20040216186A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and  
; FILE REFERENCE: 045600/274146  
; CURRENT APPLICATION NUMBER: US/10/783,417  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,806  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 735  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-783-417-2

Query Match 84.9%; Score 3318; DB 5; Length 735;  
Best Local Similarity 87.1%; Pred. No. 1.9e-248;  
Matches 639; Conservative 31; Mismatches 60; Indels 4; Gaps 3;  
Qy 1 MNQNN-NNEYEIIDSKNLSYPSNRNIDHSRYPTNNPQLQNTYKELNMCQNTQYX 59  
Db 1 MNQNNNNEYEIIDSHTSPYFFNRNSNDSRYPTNNPQLQNTYKELNMCQNTQYX 60  
Qy 60 DNFETPASADTIAAVSAGTIYVSGTLLAGIGLTSISGPIGIIIGAIISFGTITVFWPAG 119  
Db 61 DNFETPASADTIAAVSAGTIYVSGTLLAGIGLTSISGPIGIIIGAIISFGTITVFWPAG 120

Qy 120 EQDKTWTQFTKMGEIFVDTPLETSIKQLKQLTLEGFRQILQSYNTALDDWRKLRLOAP 179  
 Db 121 EQDKTWTQFTKMGEIFVDTPLETSIKQLKQLTLEGFRQILQSYNTALDDWRKLRLOAP 180  
 Qy 180 GLPSSALQAAALTLKIRFENVHNDPIREIPGFOLETYKTLPLPIYAQAANFHLNLLQOG 239  
 Db 181 GLPSSALQAAALTLKIRFENVHNDPIREIPGFOLETYKTLPLPIYAQAANFHLNLLQOG 240  
 Qy 240 AELADEWNADHPQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGNKLREPNRW 299  
 Db 241 AELADEWNADHPQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGNKLREPNRW 300  
 Qy 300 SIFNDYRYMTITVLDITIAQSFYDIKRYKDSIG--RIGGKTELREIYTTTEINFDRLT 357  
 Db 301 SIFNDYRYMTITVLDITIAQSFYDIKRYKDSIG--RIGGKTELREIYTTTEINFDRLT 360  
 Qy 358 YLEIQPNLAIMEYNLTSGRLRFLDELIFETKNETYGNRLVGIANRSTYATTGTEI 417  
 Db 361 QLRVQPNLAIMEYNLTSGRLRFLDELIFETKNETYGNRLVGIANRSTYATTGTEI 420  
 Qy 418 IYGBERTGPTTKLIPESYKVSIVTDQVTPPTSPFPNIYFTINOIELYLNNSPSNKITY 477  
 Db 421 LYGBERTGPTTKLIPESYKVSIVTDQVTPPTSPFPNIYFTINOIELYLNNSPSNKITY 479  
 Qy 478 SAGNLNDKKTTFQFPVKCKPIINPNCPLSYNSYSHILSQFSLFNYSYKIGLALNI 537  
 Db 480 SAGNLNDKKTTFQFPVKCKPIINPNCPLSYNSYSHILSQFSLFNYSYKIGLALNI 539  
 Qy 538 LYTGALGWTSSVNRNNAISDKIITMIPAKGNLSLDTNSKVIIEGPGHGGNLVYLOQGR 597  
 Db 540 LDVTGLGWTSSVNRNNAISDKIITMIPAKGNLSLDTNSKVIIEGPGHGGNLVYLOQGR 599  
 Qy 598 LEITCRPNSTQSYIRLRYATNGAGNTLPNISITIPGVIGIPORLNNTPSGTNNYLNQ 657  
 Db 600 LEITCRPNSTQSYIRLRYATNGAGNTLPNISITIPGVIGIPORLNNTPSGTNNYLNQ 659  
 Qy 658 YGDFGYQFPSTVTLPLNRNIPFIPNRAVNSNLIIDKIEFIPITSSVRQNRKQKLET 717  
 Db 660 YGDFGYQFPSTVTLPLNRNIPFIPNRAVNSNLIIDKIEFIPITSSVRQNRKQKLET 719  
 Qy 718 IQTKINTFFTNHTK 731  
 Db 720 IQTKINTFFTNHTK 733

## RESULT 4

US-10-782-141-12  
 ; Sequence 12, Application US/10782141  
 ; Publication No. US20040197917A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
 ; FILE REFERENCE: 045600/274143  
 ; CURRENT APPLICATION NUMBER: US/10782,141  
 ; CURRENT FILING DATE: 2004-02-20  
 ; PRIOR APPLICATION NUMBER: 60/448,632  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 12  
 ; LENGTH: 1180  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-141-12

Query Match 29.6%; Score 1158; DB 4; Length 1180;  
 Best Local Similarity 37.3%; Pred. No. 2e-80;

Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;  
 Qy 5 NNNEYEIDS--KNLSYFSNRNIDHSRYPTNNPNQPLQNTNYKEWLNMCQGTQYGNF 62  
 Db 6 NKNEYETLNASQKLNISNN-----YTRYPIENSFKQLQSTNYKDLNMCQONQYGGDF 61  
 Qy 63 ETPASADTAAVSAGTIVSGTLGAGIGLTSISGPIGIIIGAIISFGTLITVFPAGBQD 122  
 Db 62 ETFIDS---GELSAYTIWGTVLGTGFTT---PLGL---ALIGFGTLIPVLPFAQDQS 111  
 Qy 123 KTVMTQFIKMGEIFVDTPLETSIKQLKQLTLEGFRQILQSYNTALDDWRKLRLOAPGLP 182  
 Db 112 NT-MSDFITQKNIIKKEIASTYISNANKILNRSFNVISITHNLKWE-----NNPNQ 165  
 Qy 183 PSSALQAAALTLKIRFENVHNDPIREIP--GFQLETYKTLPLPIYAQAANFHLNLLQOG 240  
 Db 166 NTQDVRTQIQIVHVFQNVIPELVNSCPPNPSDCDYNNILVSSYAQAANLHLTVLNOAV 225  
 Qy 241 ELADEWNADHPQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGNKLREPNR----- 295  
 Db 226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTKAIEDYTNVCVTYKGLNLIKTTPDSNLD 284  
 Qy 296 -NMEWSIFNDYRYMTITVLDITIAQSFYDIKRYKDSIGRIGGKTELREIYTTTEINF 354  
 Db 285 GNINWNTYNTYRTKMTTAVLDLVALFNYDVGKPI-----GVQSELTREIYQV-LNFE 337  
 Qy 355 RLTYLEIQPNLAIMEYNLTSGRLRFLDELIFETKNETYGNRLVGIANRSTYA--- 411  
 Db 338 ESPKYY--DFQYQEDSLTRP-HLFTWLSLNFYEKAQITPNNFP-TSHYMMFHYTLDN 393  
 Qy 412 TTGTEIYIGBRTGPTTKLIPESYKVSIVTDQVTPPTSPFPNIYFTINOIELYLNNSP 471  
 Db 394 ISQSSVFGNHNVTDLKSL--GLATNIYIFLLNVLSDNKNLYNNISQWDFITNGT 451  
 Qy 472 ---SNKLTYSAGNLNDKKTTFQFPVKCKPIINPNCPLSYNSYSHILSQFSLFNY- 527  
 Db 452 RLKEKLT-AGSQGITVDVKNIFGLFILKRRNQGNPTLFTYDNTSHILLSFKSLSIP 510  
 Qy 528 -SYKIGLALNLTGALGWTSSVNRNNAISDKIITMIPAKGNLSLDTNSKVIIEGPGHTG 586  
 Db 511 ATYK----TQVYTF--WTHSSVDPKNTIYTHLTQIPAVKANSLGTASKVQPGHTG 563  
 Qy 587 GNLVYLOQGRLEITCRPNSTQSYIRLRYATNGAGNTLPNISITIPGVIGIPORLNN 646  
 Db 564 GDLI--DFKDFKITCQHSNFQSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620  
 Qy 647 TEGTNNYNNLYQDGYGFQFPSTVTLPLNRNIPFIPNRAV--SNSILIDKIEFIPITSS 705  
 Db 621 TFGTDYTNLKYKDFQYLEFNSVEVKFAPNQNISLVFNRSQVYNTTTLVDKIEFLPITRS 680  
 Qy 706 VRQNRKQKLETQTKINTFTTHTKNTLNIETATNYDID 744  
 Db 681 IREDREKQKLETQQIINTFYANPKYNTLOSELTDYDID 719

## RESULT 5

US-10-782-096-14  
 ; Sequence 14, Application US/10782096  
 ; Publication No. US20040210964A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and  
 ; FILE REFERENCE: 045600/274148  
 ; CURRENT APPLICATION NUMBER: US/10782,096  
 ; CURRENT FILING DATE: 2004-02-19  
 ; PRIOR APPLICATION NUMBER: 60/448,633  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-096-14

Query Match      29.6%; Score 1158; DB 4; Length 1180;
Best Local Similarity 37.3%; Pred. No. 2e-80;
Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;

QY  5 NNNEYEIIIDS--KNLSYPSNRNIDHSRYPTNNPNQPLQNTNYKWLNMCGNTQYGDNF 62
DB  6 NKNEYETINASQKKNISNN---YTRYPIENSFKQLQSTNYKWLNMCGNQOYGGDF 61

QY  63 ETFSADTIAAVSAGTIVSGTLLAGIGLTSISGPIIGAIISFGTLITVFWPAGSD 122
DB  62 ETFIDS---GELSAVTVVGTGTGFGFTT---PLGL---ALIGFGTLIPVLPAQDQS 111

QY  123 KTVWTFQIKMGEIFVDTPLTESIKQLKLTLEGFRQILQSYNTALDDWRKLRQAQGLP 182
DB  112 NT-WSDFITQTKNIKKIETASTVISNANKILNRSFNVISYHNLKTWE-----NNPNPQ 165

QY  183 PSSALQQAALTUKIRFENVHNDFIREIP--GFQLETYKTLPIYAAANFHLNLLQGA 240
DB  166 NTQDVRTQIQLVHYHFQNVIPELVNSCPNPSDCDYNYILVSSYAQAANLHLTVLNAQV 225

QY  241 ELADEWNADIHPSQIEPNAGTSDYYKLLKENIPKYSNYCANTYREGNKLNRNP--- 295
DB  226 KFEAYLKNRQFDYLEP-LPTAIDYVPLTKAIEDYTNVCVTTYKKGKLNLIKTPDSNLD 284

QY  296 -NMRWSIFNDYRYMTITVLDITIAQSFYDIKRYKDSIGRIGGKIKTELTREIYTFEINF 354
DB  285 GNINWNTYRTKMTITAVLDVALPFDYVGVKYP-----GVQSELTRIYQV-LNFE 337

QY  355 RLTYLEIQNLAIMENYLRSGRLPSFLDELIFVTKNETYGNRLVGIANNRSTYA--- 411
DB  338 ESPYKY--DFQYQEDSLTRRP-HLFTWLDLSNFEKAKQTPNNFF-TSHYNMFHYTLDN 393

QY  412 TTGTEIIGERTGPTTKTLIPESYKVSIVTDQVTPSPPPNIYFTINQIELYLNNSP 471
DB  394 ISQSSVFGNHNVTDKLSL--GLATNIYIFLLNVISLDNKYLDYNNISKMDFFITNGT 451

QY  472 ---SNKLYSAGNLSNDKKTDFQFPVKCKPFIINPNCLPSYNSYSHILSPKLSIP 527
DB  452 RLLEKELT-AGSQIITVDYVKNIFGLPILKRENQGNPTLFPTYDNYSHILSPKLSIP 510

QY  528 -SVKIGLALNLYTGALGWTSSVNRNNAISDKIITMIPAIGNSLDTNSKVIKPGHGT 586
DB  511 ATYK-----TQVYTFEA--WTHSSVDPKNTIYTHLTQIPAVKANSLSGTASKVQVPGHGT 563

QY  587 GNLVYLOSQRLEITCTPTNSTQSYVIRLYRATNGAGTLPNLSITIPGVIGIPQRLNN 646
DB  564 GDLI--DFKDHFKITCOHNSFOQSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620

QY  647 TFSGTNNYNNQYDGFQFPSPVTPLNRPPIFNRADV-SNSILIIDKIEPIPTSS 705
DB  621 TFSGTDYTNLYKDFQYLEFSNEVKAPNQNSLVFNRSVDYVNTVTLIDKIEPLPTRS 680

QY  706 VQNRKQKLETTQTKINTFTTNTKNTLNIEATNYDID 744
DB  681 IREDREKQKLETVQOIINTFYANPKNTLQSELTDYDID 719

RESULT 6
US-10-782-570-10
; Sequence 10, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.

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RESULT 7
US-10-783-417-8
; Sequence 8, Application US/10783417
; Publication No. US20040216186A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274146
; CURRENT APPLICATION NUMBER: US/10/783,417
; PRIOR FILING DATE: 2004-02-20
; PRIOR FILING DATE: 2004-02-20
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-783-417-8

Query Match          29.6%; Score 1158; DB 5; Length 1180;
Best Local Similarity 37.3%; Pred. No. 2e-80;
Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;

Qy      5 NNNEYEIDS--KNLSYPSNRNIDHSRYPTNNPQNPLQNTNYKEWLNMCQNTQYGDNF 62
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
6 NKNEYETLNASQKLNLSNN---YTRYPIENSFKQLQSTNYKDWLNMCQNOQYGGDF 61

Qy      63 ETPASADTIAAVSAGTIVSGTLGAGIGLTSISGPIGIIAISFGTLITVFWPAGEQD 122
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
62 ETFIDS---GELSAYTIWVGTLTGFGFTT---PLGL---ALIGFGTLIPVLPFAQDQS 111

Qy      123 KTWVTQFIKGEIFVDPTPLTESIKQLKLTLEGFRQLQSYNTALDDWRKLRQAQCLP 182
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
112 NT-WSDFITQTKNIKKKIASYISNANKILNRSFNISTVYHNLKTWE-----NNPNPQ 165

Qy      183 PSSALQQAALTALKIRFENVHDFIREIP--GFQLETYTKLLLPYAAQANFLNLQQA 240
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
166 NTQDVRTQIQLVHVFQNVIPELVNSCPNPSCDYNNILVSSYAQAANLHLTVLQAV 225

Qy      241 ELADEWNADIHPISOEPNAGTSDDYKLLKENIPKYSNYCANTYREGINKLRNP----- 295
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTAKAIDYNYCVTYTKGGLNLIKTTPDNSLD 284

Qy      296 -NMRWSIFNDYRYRMTITVLDTTAQFSFYDIKRYKDSIGRIGGKLTREIYTFEINF 354
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
285 GNINWNTYRTKMTTAVLDLVALFPNYDVGYKPI-----GVQSELTRIIYQV-LNFE 337

Qy      355 RLTYLEIQPNLAIMEYNLTRGLRFLSFDELIFTYTKNETVGNRLVGTANRRTYA--- 411
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
338 ESPKYV--DFQVQEDSLTRRP-HLFTWLDLSNFEYKAQTTPNNFF-TSHYNMHYTLDN 393

Qy      412 TTGTEIIVGERTGPTTKTLIPESYKVSIVTDQVTPTPFPPIYFTINOIELYLNNSP 471
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
394 ISQKSSVFGNHNVTDLKSL--GLATNIYIFLLNVLSDNKLNDYNNISKQDFFITNGT 451

Qy      472 ---SNKLTYSAGGNLSNDKKTTFDQFPVKQDCKPIINPCLPSYNSYSHILSOFSLFNY- 527
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
452 RLLEKELT-AGSGQITVDVNNKIFGLPILKRENGQNPFTLPPTYDNYSHILSFIKLSIP 510

Qy      528 -SYKIGALNLTTCALGTHSSVNRNNAISDKIITMIPAIGNSLDTNSKIVSGPGHTG 586
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
511 ATYK-----TQVYTF--WTHSSVDPKNTIYTHLTQTQIPAVKANSLGTSKRVQVPGHTG 563

Qy      587 GNLVYLOSQRLTCTRPNSTQSYVILRVATGAGNTLNLISLTIPGVIGIPQRLNN 646
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
564 GDLI--DFKHFKITCOHNSFQSYFIRIRVANSNGSANTRAVINLSIPGVAEL-GMALNP 620
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RESULT 8
US-10-781-979-14
; Sequence 14, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR FILING DATE: 2004-02-20
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-14

Query Match          29.6%; Score 1158; DB 5; Length 1180;
Best Local Similarity 37.3%; Pred. No. 2e-80;
Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;

Qy      5 NNNEYEIDS--KNLSYPSNRNIDHSRYPTNNPQNPLQNTNYKEWLNMCQNTQYGDNF 62
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
6 NKNEYETLNASQKLNLSNN---YTRYPIENSFKQLQSTNYKDWLNMCQNOQYGGDF 61

Qy      63 ETPASADTIAAVSAGTIVSGTLGAGIGLTSISGPIGIIAISFGTLITVFWPAGEQD 122
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
62 ETFIDS---GELSAYTIWVGTLTGFGFTT---PLGL---ALIGFGTLIPVLPFAQDQS 111

Qy      123 KTWVTQFIKGEIFVDPTPLTESIKQLKLTLEGFRQLQSYNTALDDWRKLRQAQCLP 182
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
112 NT-WSDFITQTKNIKKKIASYISNANKILNRSFNISTVYHNLKTWE-----NNPNPQ 165

Qy      183 PSSALQQAALTALKIRFENVHDFIREIP--GFQLETYTKLLLPYAAQANFLNLQQA 240
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
166 NTQDVRTQIQLVHVFQNVIPELVNSCPNPSCDYNNILVSSYAQAANLHLTVLQAV 225

Qy      241 ELADEWNADIHPISOEPNAGTSDDYKLLKENIPKYSNYCANTYREGINKLRNP----- 295
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTAKAIDYNYCVTYTKGGLNLIKTTPDNSLD 284

Qy      296 -NMRWSIFNDYRYRMTITVLDTTAQFSFYDIKRYKDSIGRIGGKLTREIYTFEINF 354
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
285 GNINWNTYRTKMTTAVLDLVALFPNYDVGYKPI-----GVQSELTRIIYQV-LNFE 337

Qy      355 RLTYLEIQPNLAIMEYNLTRGLRFLSFDELIFTYTKNETVGNRLVGTANRRTYA--- 411
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
338 ESPKYV--DFQVQEDSLTRRP-HLFTWLDLSNFEYKAQTTPNNFF-TSHYNMHYTLDN 393

Qy      412 TTGTEIIVGERTGPTTKTLIPESYKVSIVTDQVTPTPFPPIYFTINOIELYLNNSP 471
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
394 ISQKSSVFGNHNVTDLKSL--GLATNIYIFLLNVLSDNKLNDYNNISKQDFFITNGT 451

Qy      472 ---SNKLTYSAGGNLSNDKKTTFDQFPVKQDCKPIINPCLPSYNSYSHILSOFSLFNY- 527
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
452 RLLEKELT-AGSGQITVDVNNKIFGLPILKRENGQNPFTLPPTYDNYSHILSFIKLSIP 510

Qy      528 -SYKIGALNLTTCALGTHSSVNRNNAISDKIITMIPAIGNSLDTNSKIVSGPGHTG 586
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
511 ATYK-----TQVYTF--WTHSSVDPKNTIYTHLTQTQIPAVKANSLGTSKRVQVPGHTG 563

Qy      587 GNLVYLOSQRLTCTRPNSTQSYVILRVATGAGNTLNLISLTIPGVIGIPQRLNN 646
Db      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
564 GDLI--DFKHFKITCOHNSFQSYFIRIRVANSNGSANTRAVINLSIPGVAEL-GMALNP 620
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QY 587 GNLVYLOSQRLEITCRTPNSTQSYIRLRYATNGAGNTLPLNLSLITPGVIGIPPORLNN 646  
Db 564 GDLI--DFKDFKITCQHSNFQSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620  
QY 647 TFGSTNNNOYGDGFGYFQFPSTVTLPLNRNIPFNRADV-SNSILIIDKISFIPITSS 705  
Db 621 TFSGTDYTNLYKDFOYLSEFNEVKFAPNQNISLVFNRSVYNTTTLVIDKIEFLPITRS 680  
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RESULT 9  
US-09-756-526A-4  
; Sequence 4, Application US/09756526A  
; Patent No. US20020038005A1  
; GENERAL INFORMATION:  
; APPLICANT: Jana, Wojciechowska  
; APPLICANT: Evgeny, Lewitin  
; APPLICANT: Ludmila, Revina  
; APPLICANT: Igor, Zalunin  
; APPLICANT: Galina, Chestukhina  
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR  
; FILE REFERENCE: S-30913A  
; CURRENT APPLICATION NUMBER: US/09/756,526A  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: US 60/175,158  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 1109  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-09-756-526A-4  
Query Match 23.1%; Score 901; DB 3; Length 1109;  
Best Local Similarity 34.2%; Pred. No. 1.6e-60;  
Matches 240; Conservative 106; Mismatches 242; Indels 114; Gaps 27;  
QY 67 SADIATAVSAGTIVSGTLGAGIGLTSISGPIGIIGAIISFGTLITVFWPAGEQD-KTV 125  
Db 28 SSDTAVVVSAGIVVVGITLT---AFASFVNP---GVVLISFGTLAPVLPDPDEEDPKKI 80  
QY 126 WTOPIKMGEIFVDTPLTESIKQLQTLQEGFRQILQSYNTALDDWRKLRLOAPGLPPSS 195  
Db 81 WSQFMKHGEDLLNQITISTAVKEIALAHNLGFKDVLTYTTERAFNDWKR-----NPSA 131  
QY 186 ALQQAALTLKIRFENVHNDPIREIPGQLETYKTLPIYAQAANPHNLNLOQGAELADE 245  
Db 132 --NTARLVQSORENAHFNFVSNPQLQPTDYDTLLSCYTEAANLHNLHLLHGGVQFADQ 198  
QY 246 WNADIHPSQIEPNAGTSDDYYKLLKENIPKSYNCANTYREGNKLKRNPNRWSIFNDY 305  
Db 189 WNADQPHSPMLKSSGT---YDELLVYIEKYNYCTKTVHKLNLHKLSEKIKTWDAYNTY 245  
QY 306 RRYMTITVLDTIAQSFYDIKRYKDSIGRIGGIKTELTRTYTTEINFDRLTYLEIQPNL 365  
Db 246 RREMTLIVLDVATFPFYDIRFP-----RGVELELTREVYTS-----LDHLTRPPG- 292  
QY 366 AIMEYNLTRSGLRFLSFDELIFYTKNETYGNRLVGIANNRSTYATTGTEI-----IYG 420  
Db 293 -----LFTWLSDIELYTESVAEGDYLSGI-----RESKYTTGNQFTMKNIYG 335  
QY 421. ERTGPPPTK-----TLIPESYKVISVTRQVTPSPPNIFTNQIELYLNNSPSNK 474  
Db 336 N-----TNRLSKQILITLPGE-FWTHLS:NRPFQTIAGINKLYSLIQKI---VFTTFKND 386

QY 475 LTVSAGNLSND---KKTTFDQFPVKCKOCKPIINPNCLPSYNS--YSHILSOFSLFNYSY 529  
Db 387 NEYQKNFNVNQNEPQETNY-----PNDYCGSNSQRKPNLHSHFPLIIHKL 433  
QY 530 KIGLALNLYTGCALGTHSSVNRNNAISDKLIITMIPAIGNSLDTNSKVIEGCHTGNNL 589  
Db 434 EFAEYFHSIF--ALGWTNHSVNSQNLISSESVTQPLVKAYEV-TNNSVIRGGFTGGDL 490  
QY 590 VYLOSQRLEITCRTPNSTQSYIRLRYATNGAGNTLPLNLSLITPGVIGIPPORLNTFS 649  
Db 491 IELRD--KCSIKCKA--SSLKCTAISLFAANNAIAVSDIVDGSAGVL-----LQPTFS 541  
QY 650 GTNNYN-----LOYGDGFGYFQFPSTVTLPLNRNIPFNRAD--VSNLSILIIDKISFPI 702  
Db 542 RKGNNFTQDNLNYKDFQYHTLLVDIELPESEIHLKREDDYBEGVILLIDKLEFKPI 601  
QY 703 TSSVRQNRQKLEITQTKINTFTNHTKNTLNIEATNYDID 744  
Db 602 DENY---TNEMNLEKAKKAVNVLFINAT-NALKMDVTDYHID 639  
RESULT 10  
US-10-345-020-4  
; Sequence 4, Application US/10345020  
; Publication No. US20030150018A1  
; GENERAL INFORMATION:  
; APPLICANT: Jana, Wojciechowska  
; APPLICANT: Evgeny, Lewitin  
; APPLICANT: Ludmila, Revina  
; APPLICANT: Igor, Zalunin  
; APPLICANT: Galina, Chestukhina  
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR  
; FILE REFERENCE: S-30913B  
; CURRENT APPLICATION NUMBER: US/10/345,020  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/175,158  
; PRIOR FILING DATE: 2000-01-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 1109  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-345-020-4  
Query Match 23.1%; Score 901; DB 4; Length 1109;  
Best Local Similarity 34.2%; Pred. No. 1.6e-60;  
Matches 240; Conservative 106; Mismatches 242; Indels 114; Gaps 27;  
QY 67 SADIATAVSAGTIVSGTLGAGIGLTSISGPIGIIGAIISFGTLITVFWPAGEQD-KTV 125  
Db 28 SSDTAVVVSAGIVVVGITLT---AFASFVNP---GVVLISFGTLAPVLPDPDEEDPKKI 80  
QY 126 WTOPIKMGEIFVDTPLTESIKQLQTLQEGFRQILQSYNTALDDWRKLRLOAPGLPPSS 185  
Db 81 WSQFMKHGEDLLNQITISTAVKEIALAHNLGFKDVLTYTTERAFNDWKR-----NPSA 131  
QY 186 ALQQAALTLKIRFENVHNDPIREIPGQLETYKTLPIYAQAANPHNLNLOQGAELADE 245  
Db 132 --NTARLVQSORENAHFNFVSNPQLQPTDYDTLLSCYTEAANLHNLHLLHGGVQFADQ 188  
QY 246 WNADIHPSQIEPNAGTSDDYYKLLKENIPKSYNCANTYREGNKLKRNPNRWSIFNDY 305  
Db 189 WNADQPHSPMLKSSGT---YDELLVYIEKYNYCTKTVHKLNLHKLSEKIKTWDAYNTY 245  
QY 306 RRYMTITVLDTIAQSFYDIKRYKDSIGRIGGIKTELTRTYTTEINFDRLTYLEIQPNL 365  
Db 246 RREMTLIVLDVATFPFYDIRFP-----RGVELELTREVYTS-----LDHLTRPPG- 292  
QY 366 AIMEYNLTRSGLRFLSFDELIFYTKNETYGNRLVGIANNRSTYATTGTEI-----IYG 420  
Db 293 -----LFTWLSDIELYTESVAEGDYLSGI-----RESKYTTGNQFTMKNIYG 335





Db 164 --THANAKAVHDLFTTLEPIIDKDMLKNNASRIPT-----LPAYAQIATWHLNLLKH 216  
Qy 239 GAELADEWNADIHPSQIEPNAGTSDDYK--LLKENIPKYSNYCANTYREGNLKLRNEPNM 297  
Db 217 AATYNIW---LQNGQINPSTFNSSNYQGYLKRKIQEYTDYCIQTYNAGLTWIRTNTNA 273  
Qy 298 RWSIFNDYRYMTITVLDITIAQSFYDIKRYKDSIGRIGIKTELREIYTTTINPDRLT 357  
Db 274 TWMNYTYRLEMILTVDLAIAPNDYDEKYP-----GVKSELIREVY--TWNVSDTFR 326  
Qy 358 YLEIQPNLAIMEVNLTRSGRLFSFLDELIFYTKN-----ETY-----GNRLVGIANRN 406  
Db 327 -----TITELNGLTRNP--TLFTWINQGRFYTRNSRDILDPYDIFSFQGNMA----- 373  
Qy 407 RSTYATGTETIYGERG---PPTTKTILIPESY-----KVSIVTDQVTPTSPPNIYFT 459  
Db 374 -FTHTNDNRNIIGAVHGNIIISQDTSKVFPFYRNKPIDKVEIVRHE-----YSD 422  
Qy 460 INQIELYLNNSPNKLTYSAGGNLSNDKTTDFQFPVKOCKPIINPNCPLPSYNSYSHIL 519  
Db 423 IYEMIFFSNS--SEVFRYSSNSTIENNYKRTDSYMPKQTK-----NEEYGHTL 471  
Qy 520 SQSFLFNYSYKIGLALNITYGALGTHSSVNRNNAISDKIITWIPAIGNSLDTNSKVI 579  
Db 472 SYIKTDNYIFSV---VRERRVAFSWHTSVDFQNTIDLDNITQIHALKALKVSSDSKIV 528  
Qy 580 EGPCHTGNLVYLOSQGRLEITCR--TPNSTQSYIIRLYATNGAGNTLNPISLTIPGVIG 638  
Db 529 KGFPGHTGGDLVILKDS--MDFRVRFKNVSRQVQVIRYATNA-----PKTTVFLTGIDT 581  
Qy 639 IPPQRLNNTFSGTNN--NLQYGDGFGYFQFPSTV-----TLPLNRNPIPFNRADV 687  
Db 582 ISVE-LPSTTSRQNPATDLTYADFGYVTPRVPNKTFEGEDTLMT-----LYGTPNH 635  
Qy 688 SNSILIIDKIEPIPTSSVRQNRKQKLETIQKINTFFTN 728  
Db 636 SYNI-YIDKIEFIPITQSVLDYTEKQNIKTQKIVNDLFVN 675  
RESULT 13  
US-10-782-096-18  
; Sequence 18, Application US/10782096  
; Publication No. US20040210964A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and  
; FILE REFERENCE: 045600/274148  
; CURRENT APPLICATION NUMBER: US/10782,096  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 675  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-096-18  
Query Match 23.0%; Score 897; DB 4; Length 675;  
Best Local Similarity 33.0%; Pred. No. 1.6e-60;  
Matches 251; Conservative 114; Mismatches 268; Indels 128; Gaps 32;  
Qy 5 NNNYEYIIDSKNLSYSPNRNIDHSRYEYTNPNQPLQNTNYSKELANCOGNTQYGNFET 64  
Db 6 NKNYEYIIDSNGFSKSNR--YSRYPLANKPNQPLQNTNYSKELANCOGNTQYGNFET 63  
Qy 65 FASADTIAAVSAGTIVSGTLLAGIGLTSISGPIIGIIGAIISFGTLITVFWPAGEQDKT 124

Db 64 FASSETIVGSAGIIVVGTMIG-----AFAAP--VLAAGIISFGTLLPIFW-QGSDPAN 114  
Qy 125 VMTQIFKGEIFVDTPLTE---SIKQLKLOTLLEGFRQILQSYNTALDDWRKLRQAPGL 181  
Db 115 VHQDLLNIG---GRPIQIEIDKNIINVLTSIVTPIKNQQLDKYQEFPPKWEPAR----- 163  
Qy 182 PSSALQQAALTLKIRFENVHN---DFIREIFGFQLETKYKTLTLLPIYAAANPHLNLQ 238  
Db 164 --THANAKAVHDLFTTLEPIIDKDMLKNNASRIPT-----LPAYAQIATWHLNLLKH 216  
Qy 239 GAELADEWNADIHPSQIEPNAGTSDDYK--LLKENIPKYSNYCANTYREGNLKLRNEPNM 297  
Db 217 AATYNIW---LQNGQINPSTFNSSNYQGYLKRKIQEYTDYCIQTYNAGLTWIRTNTNA 273  
Qy 298 RWSIFNDYRYMTITVLDITIAQSFYDIKRYKDSIGRIGIKTELREIYTTTINPDRLT 357  
Db 274 TWMNYTYRLEMILTVDLAIAPNDYDEKYP-----GVKSELIREVY--TWNVSDTFR 326  
Qy 358 YLEIQPNLAIMEVNLTRSGRLFSFLDELIFYTKN-----ETY-----GNRLVGIANRN 406  
Db 327 -----TITELNGLTRNP--TLFTWINQGRFYTRNSRDILDPYDIFSFQGNMA----- 373  
Qy 407 RSTYATGTETIYGERG---PPTTKTILIPESY-----KVSIVTDQVTPTSPPNIYFT 459  
Db 374 -FTHTNDNRNIIGAVHGNIIISQDTSKVFPFYRNKPIDKVEIVRHE-----YSD 422  
Qy 460 INQIELYLNNSPNKLTYSAGGNLSNDKTTDFQFPVKOCKPIINPNCPLPSYNSYSHIL 519  
Db 423 IYEMIFFSNS--SEVFRYSSNSTIENNYKRTDSYMPKQTK-----NEEYGHTL 471  
Qy 520 SQSFLFNYSYKIGLALNITYGALGTHSSVNRNNAISDKIITWIPAIGNSLDTNSKVI 579  
Db 472 SYIKTDNYIFSV---VRERRVAFSWHTSVDFQNTIDLDNITQIHALKALKVSSDSKIV 528  
Qy 580 EGPCHTGNLVYLOSQGRLEITCR--TPNSTQSYIIRLYATNGAGNTLNPISLTIPGVIG 638  
Db 529 KGFPGHTGGDLVILKDS--MDFRVRFKNVSRQVQVIRYATNA-----PKTTVFLTGIDT 581  
Qy 639 IPPQRLNNTFSGTNN--NLQYGDGFGYFQFPSTV-----TLPLNRNPIPFNRADV 687  
Db 582 ISVE-LPSTTSRQNPATDLTYADFGYVTPRVPNKTFEGEDTLMT-----LYGTPNH 635  
Qy 688 SNSILIIDKIEPIPTSSVRQNRKQKLETIQKINTFFTN 728  
Db 636 SYNI-YIDKIEFIPITQSVLDYTEKQNIKTQKIVNDLFVN 675  
RESULT 14  
US-10-782-570-14  
; Sequence 14, Application US/10782570  
; Publication No. US20040210965A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274144  
; CURRENT APPLICATION NUMBER: US/10782,570  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 675  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-570-14



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:51:09 ; Search time 13 Seconds  
(without alignments)  
385.437 Million cell updates/sec

Title: US-10-782-570-2

Perfect score: 3906

Sequence: 1 MNQNNNEYEIIDSKNLSYP.....FFTNHTKNTLNIEATNYDID 744

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51463 seqs, 6734788 residues

Total number of hits satisfying chosen parameters: 51463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB\_PEP.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB\_PEP.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB\_PEP.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB\_PEP.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	720	18.4	1210	7	US-11-058-727-4
2	720	18.4	1210	7	US-11-058-727-4
3	704	18.0	652	7	US-11-192-801-4
4	703	18.0	1206	7	US-11-058-727-2
5	703	18.0	1206	7	US-11-108-389-2
6	697	17.8	652	7	US-11-192-801-6
7	695	17.8	652	7	US-11-192-801-2
8	683.5	17.5	1386	7	US-11-091-643-6
9	683	17.5	653	7	US-11-192-801-8
10	683	17.5	653	7	US-11-192-801-10
11	683	17.5	653	7	US-11-192-801-12
12	683	17.5	653	7	US-11-192-801-14
13	683	17.5	653	7	US-11-192-801-16
14	683	17.5	653	7	US-11-192-801-18
15	683	17.5	653	7	US-11-192-801-20
16	683	17.5	653	7	US-11-192-801-22
17	683	17.5	653	7	US-11-192-801-24
18	683	17.5	653	7	US-11-192-801-37
19	683	17.5	653	7	US-11-192-801-39
20	679	17.4	673	7	US-11-058-727-14
21	679	17.4	673	7	US-11-108-389-14
22	674	17.3	1316	7	US-11-091-643-4
23	669	17.1	675	7	US-11-058-727-74
24	669	17.1	675	7	US-11-058-727-80
25	669	17.1	675	7	US-11-108-389-74

## ALIGNMENTS

## RESULT 1

US-11-058-727-4  
; Sequence 4, Application US/11058727  
; Publication No. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnall  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; FILE REFERENCE: 35718/287809  
; CURRENT APPLICATION NUMBER: US/11/058,727  
; PRIOR FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIOR FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1210  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-11-058-727-4

Query Match 18.4%; Score 720; DB 7; Length 1210;

Best Local Similarity 27.5%; Pred. No. 2e+46;

Matches 217; Conservative 137; Mismatches 304; Indels 132; Gaps 30;

QY 1 MNQNNNEYEIIDSKNLSYPSNRNIDHSRYPTNNPQLONTNYKSWLNNCOGN-TQYG 59

DB 1 MSPNNQNEYEIIDATPSTSVSN---DSNRYPFANEPTNALQNDYKDYKMSAGNASEYP 57

QY 60 DNFETFASATIAAASAGTIVSGTLLAGIGGLTSISGPIGIIIGAIISFGTLITVFWPAG 119

DB 58 GSPEVLVSGQD--AAKAAIDIVGKLLSGLG-----VPFVGPIVSLYQTQIDILWPSG 107

QY 120 EQDKTWTQIKWGEIPVDTPLTSTESIKQLKLTLEGFRQILQSNTALDDWRKLRQAP 179

DB 108 Q--KSQWEIFMEQVEELINQKIAFYARNKALSELGLEGNNYQLYLTALKEWKE----- 158

Sequence 80, Appl  
Sequence 82, Appl  
Sequence 82, Appl  
Sequence 42, Appl  
Sequence 48, Appl  
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Sequence 50, Appl  
Sequence 50, Appl  
Sequence 70, Appl  
Sequence 34, Appl  
Sequence 68, Appl  
Sequence 34, Appl  
Sequence 68, Appl  
Sequence 76, Appl  
Sequence 76, Appl  
Sequence 22, Appl  
Sequence 64, Appl  
Sequence 66, Appl

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27 668.5 17.1 674 7 US-11-058-727-82  
28 668.5 17.1 674 7 US-11-108-389-82  
29 668 17.1 675 7 US-11-058-727-42  
30 668 17.1 675 7 US-11-058-727-48  
31 668 17.1 675 7 US-11-108-389-42  
32 668 17.1 675 7 US-11-108-389-48  
33 667.5 17.1 674 7 US-11-058-727-50  
34 667.5 17.1 674 7 US-11-108-389-50  
35 666 17.1 673 7 US-11-058-727-70  
36 666 17.1 673 7 US-11-108-389-70  
37 665 17.0 673 7 US-11-058-727-34  
38 665 17.0 673 7 US-11-058-727-68  
39 665 17.0 673 7 US-11-108-389-34  
40 665 17.0 673 7 US-11-108-389-68  
41 664.5 17.0 674 7 US-11-058-727-76  
42 664.5 17.0 674 7 US-11-108-389-76  
43 664 17.0 673 7 US-11-058-727-22  
44 664 17.0 673 7 US-11-058-727-64  
45 664 17.0 673 7 US-11-058-727-66

```
QY 180 GLPPSALQQAALTAKIRFENVHNDPIREIPGFOLEYTKTLPIYAQAANFHLNLLQOG 239
Db 159 --NPGS--RALLDRVNRFEILDSLFTQYMPFSRVNFEVPFLTVYVYQAANLHLLLKDA 214
QY 240 AELADENADIHPSQIEPNAGTSDYYKLLKENIPKYSNYCANTYREGLNKLANEPMRW 299
Db 215 SIFGEWGW-----STTTINNYDROMKLTAEYSDHCWKYETGLAKLGTSAKQW 265
QY 300 SIFNDVRYMTITVLDIAQFSYDIKRYKDSIGRIGGKTELTRREIYTT---EINFDR 356
Db 266 VDYNQFRREMTLVLDVVALFPNYDRTYPM-----TKAQLTREYVTDPLGAVNVSSI 319
QY 357 -TYLEIQNLAIMYENLITRSLRFLSDELIFVTKNET-----YGNRLVGIANRSTY 410
Db 320 GSWYDKAPSGVIESSVIRPP-HVFDYITGLTVYTSRSISSARYIRHWAGHOISVHRIF 378
QY 411 ATTGTETIYGERTPPTTKTLIPFESYKV-SIVTDQVTPTSPPFN---IYFTINQIELY 466
Db 379 SDNIKQMYGTNQNHLSTST-PDFTNYDIYKTLSDKAVLLDIVPFGYTYIFFGMEVEFP 437
QY 467 LNNSPSNKLTYSAGNLSNDKTTDFQFPVKKCKPII-----NPNCLPSYNS 514
Db 438 MVN-----QLNTRKTLKN-PVSKD---IAGTRDSELELPPETSQDPNYES 481
QY 515 YSHILSQFSLFNYSYKIGLALNLTGTA-----LGWTHSSVNRNNAISDKIITMIPAI 567
Db 482 YSHRLCHIT-----SIPATGSTTGLVPVFSWTHRSADLINAVHSDKITQIPV 529
QY 568 KGNLSL-----DTNSKVIIEGPGHTGGLVYLOSQGRLL--EITCRTPNSTQSYVIRLYAT 619
Db 530 KVSIDLAPSGTGGPNNTVWSGPGTGGGIKVIKIRNGVISHMRVKISDINKESMRIRYAS 589
QY 620 NGAGNTLPNLSLTIPGVIGIPQRLNNTFSGTNNYNNLOYGDFGYPFPSTVTLPLNRNIP 679
Db 590 --ANNTFEYINPSEENVKS-HAOKTMNRGEALTYNKFNYATLPPIKFTTTE-----P 638
QY 680 F-----IFNRADVNSLIIIDKIEPIPTSSVRQREKOKLETIOQKINTFFNHTKNTL 734
Db 639 FITLGAIFEAEFLGIEAYIDRIEFIPVDETY---EAEQDLEAAKAVNALFTN-TKQGL 694
QY 735 NIEATNYDID 744
Db 695 RFGVTDYEVN 704
```

## RESULT 2

```
US-11-108-389-4
; Sequence 4, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 4
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-108-389-4
```

Query Match 18.4%; Score 720; DB 7; Length 1210;

Best Local Similarity 27.5%; Pred. No. 2e-46; Matches 217; Conservative 137; Mismatches 304; Indels 132; Gaps 30;

```
QY 1 MNQNNNYEIIDSKNLSYSPSNRNDHSRYPTYNPNQPLQNTYKWLNMCOGN-TQYG 59
Db 1 MSPNNQNEYEIIDAFTSTSVSN--DSNRRYPANEPTNALQNMWDYKDKLMSAGNASEYP 57
QY 60 DNFEFTASADTTAAVSAGTIIVSGTLLAGIGGUTSISGPIGIGAILIISGTLITVFPAG 119
Db 58 GSPEVLVSGQD--AAKAAIDIVKGLSLGL-----VPFVGPIVSLYTQILDILWPSG 107
QY 120 EQDKTWTQFIKMGEIFVDTPLTESI KQLKLTLEGFRQILOSNTALDDWRKLRLOAP 179
Db 108 Q--KSQWEIFMEQVEELINQKTAEBARNKALSELGGLGNYYQLYLTALSEWKE----- 158
QY 180 GLPPSALQQAALTAKIRFENVHNDPIREIPGFOLEYTKTLPIYAQAANFHLNLLQOG 239
Db 159 --NPGS--RALLDRVNRFEILDSLFTQYMPFSRVNFEVPFLTVYVYQAANLHLLLKDA 214
QY 240 AELADENADIHPSQIEPNAGTSDYYKLLKENIPKYSNYCANTYREGLNKLANEPMRW 299
Db 215 SIFGEWGW-----STTTINNYDROMKLTAEYSDHCWKYETGLAKLGTSAKQW 265
QY 300 SIFNDVRYMTITVLDIAQFSYDIKRYKDSIGRIGGKTELTRREIYTT---EINFDR 356
Db 266 VDYNQFRREMTLVLDVVALFPNYDRTYPM-----TKAQLTREYVTDPLGAVNVSSI 319
QY 357 -TYLEIQNLAIMYENLITRSLRFLSDELIFVTKNET-----YGNRLVGIANRSTY 410
Db 320 GSWYDKAPSGVIESSVIRPP-HVFDYITGLTVYTSRSISSARYIRHWAGHOISVHRIF 378
QY 411 ATTGTETIYGERTPPTTKTLIPFESYKV-SIVTDQVTPTSPPFN---IYFTINQIELY 466
Db 379 SDNIKQMYGTNQNHLSTST-PDFTNYDIYKTLSDKAVLLDIVPFGYTYIFFGMEVEFP 437
QY 467 LNNSPSNKLTYSAGNLSNDKTTDFQFPVKKCKPII-----NPNCLPSYNS 514
Db 438 MVN-----QLNTRKTLKN-PVSKD---IAGTRDSELELPPETSQDPNYES 481
QY 515 YSHILSQFSLFNYSYKIGLALNLTGTA-----LGWTHSSVNRNNAISDKIITMIPAI 567
Db 482 YSHRLCHIT-----SIPATGSTTGLVPVFSWTHRSADLINAVHSDKITQIPV 529
QY 568 KGNLSL-----DTNSKVIIEGPGHTGGLVYLOSQGRLL--EITCRTPNSTQSYVIRLYAT 619
Db 530 KVSIDLAPSGTGGPNNTVWSGPGTGGGIKVIKIRNGVISHMRVKISDINKESMRIRYAS 589
QY 620 NGAGNTLPNLSLTIPGVIGIPQRLNNTFSGTNNYNNLOYGDFGYPFPSTVTLPLNRNIP 679
Db 590 --ANNTFEYINPSEENVKS-HAOKTMNRGEALTYNKFNYATLPPIKFTTTE-----P 638
QY 680 F-----IFNRADVNSLIIIDKIEPIPTSSVRQREKOKLETIOQKINTFFNHTKNTL 734
Db 639 FITLGAIFEAEFLGIEAYIDRIEFIPVDETY---EAEQDLEAAKAVNALFTN-TKQGL 694
QY 735 NIEATNYDID 744
Db 695 RFGVTDYEVN 704
```

## RESULT 3

```
US-11-192-801-4
; Sequence 4, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
```

```

; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-11-192-801-4

```

[illegible]

```

RESULT 4
US-11-058-727-2
; Sequence 2, Application US/11058727
; Publication NO. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-058-727-2

```

[illegible]



```

Qy 518 ILSQFSLFNYSKIGLALNLYVTG-----ALGWTHTSSVNRNNAIISDKIITMIPAIGN 570
|      :|||      |||      |||      |||      |||      |||      |||      |
Db 485 RLCHIT-----SIPATGNTTGIVPVFSWTHRSADLNNTIYSDKITQIPAVKCW 532
|      :|||      |||      |||      |||      |||      |||      |||      |
Qy 571 SLDTNSKVIIEGGHGTGNLV-YLOSOG-----RLEICTETPNSTQSYYIRLRY 617
|      :|||      |||      |||      |||      |||      |||      |||      |
Db 533 DNLFPVPVKPGPHGTGGOLLQNRRSTGSVGTLFLARYGLALE-----KAGKYRVRLRY 585
|      :|||      |||      |||      |||      |||      |||      |||      |
Qy 618 ATNGAGNTLPNISLTIPGVIGIPPORLNNTSGTNNYLQYGDGFQFPPTVTILPLNRN 677
|      :|||      |||      |||      |||      |||      |||      |||      |
Db 586 ATDA-----DIVLHVNDQAQMCKTMNPG-----EDLTSTKFKVADAITTLNLTATDSS 633
|      :|||      |||      |||      |||      |||      |||      |||      |
Qy 678 IPPIFNRAVDNS-----ILIIDKIBFIPIITSVRONREKQKLETTOTKINTPFTNHKT 733
|      :|||      |||      |||      |||      |||      |||      |||      |
Db 634 LALKHLNGEDENSTLSGIYVVDRIFIPVDETY---EAEQDLEAAKKAVALFTN--TKDG 689
|      :|||      |||      |||      |||      |||      |||      |||      |
Qy 734 LNIEATNYDID 744
|      :|||      |||      |||      |||      |||      |||      |||      |
Db 690 LRPGVTDYEVN 700
|      :|||      |||      |||      |||      |||      |||      |||      |

RESULT 5
US-11-108-389-2
; Sequence 2, Application US/11108389
; Publication NO. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-11-108-389-2

```

```

Query Match      18.0%; Score 703; DB 7; Length 1206;
Best Local Similarity 27.6%; Pred.No.3.7e-45;
Matches 218; Conservative 140; Mismatches 295; Indels 138; Gaps 31;

Qy      1  MNQNNNEYIIDSKNLSYSPSNRNIDHSRYPTYNPNQPLONTNPKWLNWCOGN-TOYG 59
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1  MSPNNQNEYIIDATPSTSVSN-----DSNRYFPANEPTNALQNNMDYKYLKWSAGNASEYP 57
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      60  DNFETPASADTIAAVSAGTIVSGTLLAGIGGLTISGPIGIGHAIIISFGTLITVFPAG 119
      60  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      58  GSPEVLVSGQD--AAKAALDITVGLLSGLG-----VPPVGPIVSLYTLQIDILWPSG 107
      58  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      120  EQDKTVTQFTKMGEIFVDTPLTETSIKQLKLTLEGFRQILLOSNTALDDRRKLKRLQAP 179
      120  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      108  E--KSQWEIFMEQVEELINKIAEYARNKALSELGLGNNVQLYLTALDEWEE----- 158
      108  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      180  GLPSSALQQAALTKLIRFENVHNDPIREIEPGQLETYKTLTLLLPYAAQANFHLNLQOG 239
      180  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      159  --NPGS--RALRDVNRNFETLDSLTFTYMSFRTVNPFEVPLTVYAAANLHLLLKDA 214
      159  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Qy 240 AELADEWNADIHPISOIEPNACTSDDYKLLKENIPKYSINYCANTYREGLNKLRNEPMRW 299
Db 215 SIFGEENGW-----STTINNYYDQMKLTAEYSCHVKVYETGLAKLGTSAKW 265
Qy 300 SIFNDYRYMTITVLDTIAQSFYDIKRYKDSIGRIGGIKTELTRIYTT--EINFDR 356
Db 266 VDNQFRRMTLAVLDVVALFPNYDTRYPM-----TKAQLTRVYTDPLGAVNVSSI 319
Qy 357 -TYLEIQNLAIMBYNLRSLRFLSFDELIFYTKNETYGN-RLVGIANRRNSTY--AT 412
Db 320 GSWYDKAPSPGVIESSVIRPE-HVPDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS 378
Qy 413 TGTEI--LYGERTGPPTKTLIPESYKV-SIVTDROYTPTSPFPN--LYFTINQIELY 466
Db 379 RGSNLQMGYGNQLHSTST-FDFTNYDIYKTLSDKDAVLDDIVIPGYTYIFFGMPEVEFF 437
Qy 467 LNNSPSNKLTYSAGNLNSNDKKTDFQFPVKDKCKPIINPNCL-----PSYNSYSH 517
Db 438 MVN-----QLNNRKTLYN-PVSKDIIASTRDSLELPETSDQPNYESYSH 484
Qy 518 ILSQSFLENYSKYKGLALNLIYTG-----ALGHTHSSVNRNNAISDKIITWPAIKGN 570
Db 485 RLCHIT-----SIPATGNVTGLVPVPSWTHRSADLNNTIYSDKITQIPAVKCW 532
Qy 571 SLDTNSKVIEPGHTGGNLV-YLOSQ-----RLEITCRTPNSTQSYIIRLRY 617
Db 533 DNLFPVPVKPGHGTGDLQYNRSTGSGVTGLFLARYGLALE-----KAGKYRVRLRY 585
Qy 618 ATNGAGNTLPNISLTIPGVIGIPQORLNTPSGTNNYNLQYGDGFGYFPQSTVTLPLNRN 677
Db 586 ATDA-----DIVLHVNDQAQMPKTMNPG-----EDLTSKTFKVADAITTLNLATDSS 633
Qy 678 IPFIENRADVNS---ILIIDKIEFIPITSSVRQNRKOKLETQIKNTPTFNHTKNT 733
Db 634 LALKHNLGEDPNSILSGIVYVDRIEPIVDETY---EAEQDLEAKKAVNALFTN-TKDG 689
Qy 734 LNIENATNYDID 744
Db 690 LRPGWTDYEVN 700

RESULT 6
US-11-192-801-6
; Sequence 6, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 6
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic or
; OTHER INFORMATION: non-naturally occurring amino acid sequence encoded by SEQ ID
; FEATURE:
; NAME/KEY: PRT
; LOCATION: (1)..(652)
US-11-192-801-6

```

Query Match 17.8%; Score 697; DB 7; Length 652;

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Qy 1 MNQNNNEYEIDSKNLSYPSNRNIDHSRYPTNNPQPLQNTYKXWLNMCQ-GNTQYG 59
Db 1 MNPNRSEHDTI---KVTNPSELQTNHNOYPLADNPNSLTLEELNXYKFLRMTEDSSIEVL 57
Qy 60 DNFTFASADTIA-AVSAGTIIVSGTLLAGIGLTSISGPIGIIAGIISFTGLTVFWPA 118
Db 58 DN-----STVKDAVGTGISVVGQILGVWG-----VPFAGALTSFYQSFLNTIWP 102
Qy 119 GEQDKTVMOTFIKMGEIFVDTPLETESIKQLKLTQLEGFRQILQSYNTALDDWRKLRQA 178
Db 103 ---DADPKAPMAQVEVLIDKKIEYAKSKALAELOGLQNNFEDYVVALNSWK----- 153
Qy 179 PGLPSSALQQAALTAKIRFENVHDFIREIPGQLEYTKTLPIYAQAANFHLNLQ 238
Db 154 --TPLSLRSKRSQDRIRLFQAESHFRNSMPSFAVSKFEVLPLPTYAQAANTHLLLLKD 211
Qy 239 GAELADENADIHPSQIEPNAGTSDDDYKLLKENIPKYSNCANTYREGLNKLNEPNMR 298
Db 212 AQVFGEEWGYG-----SEDAEAFYHQKLT-QQYTDHCVMVNVNGLNGLRGSTYDA 262
Qy 299 WSIENDYRRYMTITVLDITIAQFSFYDIKRYKDSIGRIGGIKTELTRTYTTEINFDRITY 358
Db 263 WVKFNRRFEMTLVLDLIVLFPFYDRLYSK-----GVKTELTRDITDPI-FSLNTL 315
Qy 359 LEIQPNLAIMEYNLRSGLRFLSFLDELIFYTK-----NETYGNRLVGIANRNR 407
Db 316 QEYGPTELSIENSIRKP--HLFDYLOGIEFHTRLPQGVFGKDSFNYSWGNV---VETRPS 370
Qy 408 STYATTGTEIYIGERTGPTTKLIPESYKVSIVTDROV--TPTSPPN--IYFTTNOI 463
Db 371 IGSKTITSPYGDKSTEPVQK--LSFDGQKVY---RTIANTDVAAMPNGKVLGVTKV 424
Qy 464 ELYLNNSPSNKL---TVSA---CGNLSNDKTTDFOPPVKKDCKPIINPNCPLSYNSVSH 517
Db 425 DFSQYDDQKNETSTQTYDSKRNNGHVSQAQSID--QLPETTDEPL-----EKAYSH 474
Qy 518 ILSQSFNFYSYKIGLALNLYTGALGHTSHSVNRNNAISDKIITMIPAKGNSLDTNSK 577
Db 475 QLYNAECLMQDRGTTI--PPFT---WTHRSVDVFNTIDAETITQLPVVKAYALSSGAS 528
Qy 578 VIEPGHTGGLNLYLO-----SQGLEITCTPNTSTQSYIRLRVATGAGNTLPIISLTI 633
Db 529 IIEGPGFTGGLLFLKESNSIAKFKVTLNSAALLQRYVRIRYAST-----TNLRLFV 582
Qy 634 PGVIGIPQRLNNTFSGTNYN-----NLQYGDGFYQFPSTVTLPLNRNIPFIENRAD 686
Db 583 -----QNSNDFLVIYINKTNKDDDLTYQTFDLATNNSMFGSGDKNELIIGAESF 634
Qy 687 VNSILIIDKIEFTPI 702
Db 635 VSNEKIYIDKIEFTPI 650

```

## RESULT 7

```

US-11-192-801-2
; Sequence 2, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 652
; TYPE: PRT

```

```

; ORGANISM: Bacillus thuringiensis
US-11-192-801-2

```

```

Query Match 17.8%; Score 695; DB 7; Length 652;
Best Local Similarity 28.4%; Pred. No. 6.1e-45;
Matches 209; Conservative 121; Mismatches 286; Indels 120; Gaps 28;

```

```

Qy 1 MNQNNNEYEIDSKNLSYPSNRNIDHSRYPTNNPQPLQNTYKXWLNMCQ-GNTQYG 59
Db 1 MNPNRSEHDTI---KVTNPSELQTNHNOYPLADNPNSLTLEELNXYKFLRMTEDSSIEVL 57
Qy 60 DNFTFASADTIA-AVSAGTIIVSGTLLAGIGLTSISGPIGIIAGIISFTGLTVFWPA 118
Db 58 DN-----STVKDAVGTGISVVGQILGVWG-----VPFAGALTSFYQSFLNTIWP 102
Qy 119 GEQDKTVMOTFIKMGEIFVDTPLETESIKQLKLTQLEGFRQILQSYNTALDDWRKLRQA 178
Db 103 ---DADPKAPMAQVEVLIDKKIEYAKSKALAELOGLQNNFEDYVVALNSWK----- 153
Qy 179 PGLPSSALQQAALTAKIRFENVHDFIREIPGQLEYTKTLPIYAQAANFHLNLQ 238
Db 154 --TPLSLRSKRSQDRIRLFQAESHFRNSMPSFAVSKFEVLPLPTYAQAANTHLLLLKD 211
Qy 239 GAELADENADIHPSQIEPNAGTSDDDYKLLKENIPKYSNCANTYREGLNKLNEPNMR 298
Db 212 AQVFGEEWGYG-----SEDAEAFYHQKLT-QQYTDHCVMVNVNGLNGLRGSTYDA 262
Qy 299 WSIENDYRRYMTITVLDITIAQFSFYDIKRYKDSIGRIGGIKTELTRTYTTEINFDRITY 358
Db 263 WVKFNRRFEMTLVLDLIVLFPFYDRLYSK-----GVKTELTRDITDPI-FSLNTL 315
Qy 359 LEIQPNLAIMEYNLRSGLRFLSFLDELIFYTK-----NETYGNRLVGIANRNR 407
Db 316 QEYGPTELSIENSIRKP--HLFDYLOGIEFHTRLPQGVFGKDSFNYSWGNV---VETRPS 370
Qy 408 STYATTGTEIYIGERTGPTTKLIPESYKVSIVTDROV--TPTSPPN--IYFTTNOI 463
Db 371 IGSKTITSPYGDKSTEPVQK--LSFDGQKVY---RTIANTDVAAMPNGKVLGVTKV 424
Qy 464 ELYLNNSPSNKL---TVSA---CGNLSNDKTTDFOPPVKKDCKPIINPNCPLSYNSVSH 517
Db 425 DFSQYDDQKNETSTQTYDSKRNNGHVSQAQSID--QLPETTDEPL-----EKAYSH 474
Qy 518 ILSQSFNFYSYKIGLALNLYTGALGHTSHSVNRNNAISDKIITMIPAKGNSLDTNSK 577
Db 475 QLYNAECLMQDRGTTI--PPFT---WTHRSVDVFNTIDAETITQLPVVKAYALSSGAS 528
Qy 578 VIEPGHTGGLNLYLO-----SQGLEITCTPNTSTQSYIRLRVATGAGNTLPIISLTI 633
Db 529 IIEGPGFTGGLLFLKESNSIAKFKVTLNSAALLQRYVRIRYAST-----TNLRLFV 582
Qy 634 PGVIGIPQRLNNTFSGTNYN-----NLQYGDGFYQFPSTVTLPLNRNIPFIENRAD 686
Db 583 -----QNSNDFLVIYINKTNKDDDLTYQTFDLATNNSMFGSGDKNELIIGAESF 634
Qy 687 VNSILIIDKIEFTPI 702
Db 635 VSNEKIYIDKIEFTPI 650

```

## RESULT 8

```

US-11-091-643-6
; Sequence 6, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or

```





Db 104 --DADPWKAFMAQVEVLIDKKIEYAKSKALAEQLQGNFFEDYVNALNSWK-----154

Qy 180 GLPPSSALQQAALTLKIRFENVHDFIREIPGQLETKYKLLLPPIYAQAANFHLNLLQOG 239

Db 155 -TPLSLRSKRSQDRIRELFSQAESHFRNSPFAVSKFEVLFLPTTYAQAANTHLLLLKDA 213

Qy 240 AELADEWNADIHPSQIEPNAGTSD--YYKLLKENIPKYSNYCANTYREGLNKLRNEPN 296

Db 214 QVGEENGWY-----STVDKAVGTGIVSVQQLGVVG-----VFFAGALTSFQSFNTWPS-103

Qy 297 MRWSIFNDYRRYMTITVLDTIAQFSFYDIKRYKDSIGRIGGIKTELTRIETTYTTEINFDR 356

Db 262 DAWKFNFRREMTLTVLDLIVLPFPYDIRLYSK-----GVKTELTRDIFTDPI-FLLT 314

Qy 357 TYLEIQNLAIMENYLRSGRLPFLDELIFYTK-----NETYGNRLVGIANR 405

Db 315 TLOKYGPTFLSIENSIRKP--HLFDYLGQIEFHTRLPAGYFGKDSFNYWSGNY---VETR 369

Qy 406 NRSTYATTGTEIYGBERTGPTTKTLIPFESYKVSIVTDROV--TPTSPPPN--IYFTIN 461

Db 370 PSIGSSKTIITSPYGDKSTEPVK--LSFDGQKYY-----RTIANTDVAWPNGKVLGV 423

Qy 462 QIELYLNNSPNKL---TYSA---GGLNSNDKKTDPFPVKKCKPIINPNCLPSYNS 515

Db 424 KVDPSQYDDQKNETSTQTYDSKRNGHVSAQDSID--QLPPTTDEPL-----EKAY 473

Qy 516 SHILSQFSLFNYKYKIGLAINILYTGALGHTHSSVNRNNAISDKIITMIPAIGNSLDTN 575

Db 474 SHQLNVAECFLMDRRGTI--PFFT-----WTHRSVDFNTIDAETITQLPVPVKAYALS 527

Qy 576 SKVIEGPGHTGGLNVLQO---SQGRLEITCRTPNSTQSYIYRLRYATNGAGNTLPNIS 631

Db 528 ASIIEGPGFTGGLNLFKESNSIAKFVTLNSAALLQRYVRIRVAST-----TNLRL 581

Qy 632 TIPGVIGIPQRLNNTFSGTNYN-----NLQYGDGYFPQFPSTVTLPLNRNPIFNR 684

Db 582 FV-----QNSNDFLVIYINKTMKDDLTQYTFDLATTNSNMFGSKDKNELIIGAE 633

Qy 685 ADVNSNLIIDKIEFPI 702

Db 634 SFVSNKIIYIDKIEFIPV 651

RESULT 12

US-11-192-801-14

; Sequence 14, Application US/11192801

; Publication No. US20050273882A1

; GENERAL INFORMATION:

; APPLICANT: Romano, Charles P.

; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

; CURRENT APPLICATION NUMBER: US/11/192,801

; PRIOR FILING DATE: 2005-07-29

; PRIOR APPLICATION NUMBER: US/10/232,665

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US/09/377,466

; PRIOR FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 653

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: peptide encoded by SEQ ID NO:

; FEATURE:

; NAME/KEY: PRT

; LOCATION: (1)..(653)

; OTHER INFORMATION: Cry3Bb1 variant v11231

US-11-192-801-14

Query Match 17.5%; Score 683; DB 7; Length 653;

Best Local Similarity 28.0%; Pred. No. 4.9e-44;

Matches 207; Conservative 122; Mismatches 283; Indels 126; Gaps 28;

Qy 2 NONNNNEYEIIOSKNLSYSPSNRNIDHSRYPYTNNPNQPLONTYKWLNMCO-GNTQYGD 60

Db 3 NPNNRSEHDTI---KVTPNSELQTNHNOYPLADNPNSTLEELNYKEFLRMTEDESSTEVL 59

Qy 61 NPETPASADTIA-AVSAGTIIVSGTLLAGIGLTSISGPIGIIGAILIISFGTLITVWPAG 119

Db 60 N-----STVDKAVGTGIVSVQQLGVVG-----VFFAGALTSFQSFNTWPS-103

Qy 120 EODKTVTWFQIRKMGEIFVDTPLTESIKQLQTLQLEGFRQILOSYNTALDDWRKLKRLQAP 179

Db 104 --DADPWKAFMAQVEVLIDKKIEYAKSKALAEQLQGNFFEDYVNALNSWK-----154

Qy 180 GLPPSSALQQAALTLKIRFENVHDFIREIPGQLETKYKLLLPPIYAQAANFHLNLLQOG 239

Db 155 -TPLSLRSKRSQDRIRELFSQAESHFRNSPFAVSKFEVLFLPTTYAQAANTHLLLLKDA 213

Qy 240 AELADEWNADIHPSQIEPNAGTSD--YYKLLKENIPKYSNYCANTYREGLNKLRNEPN 296

Db 214 QVGEENGWY-----STVDKAVGTGIVSVQQLGVVG-----VFFAGALTSFQSFNTWPS-103

Qy 297 MRWSIFNDYRRYMTITVLDTIAQFSFYDIKRYKDSIGRIGGIKTELTRIETTYTTEINFDR 356

Db 262 DAWKFNFRREMTLTVLDLIVLPFPYDIRLYSK-----GVKTELTRDIFTDPI-FLLT 314

Qy 357 TYLEIQNLAIMENYLRSGRLPFLDELIFYTK-----NETYGNRLVGIANR 405

Db 315 TLOKYGPTFLSIENSIRKP--HLFDYLGQIEFHTRLPAGYFGKDSFNYWSGNY---VETR 369

Qy 406 NRSTYATTGTEIYGBERTGPTTKTLIPFESYKVSIVTDROV--TPTSPPPN--IYFTIN 461

Db 370 PSIGSSKTIITSPYGDKSTEPVK--LSFDGQKYY-----RTIANTDVAWPNGKVLGV 423

Qy 462 QIELYLNNSPNKL---TYSA---GGLNSNDKKTDPFPVKKCKPIINPNCLPSYNS 515

Db 424 KVDPSQYDDQKNETSTQTYDSKRNGHVSAQDSID--QLPPTTDEPL-----EKAY 473

Qy 516 SHILSQFSLFNYKYKIGLAINILYTGALGHTHSSVNRNNAISDKIITMIPAIGNSLDTN 575

Db 474 SHQLNVAECFLMDRRGTI--PFFT-----WTHRSVDFNTIDAETITQLPVPVKAYALS 527

Qy 576 SKVIEGPGHTGGLNVLQO---SQGRLEITCRTPNSTQSYIYRLRYATNGAGNTLPNIS 631

Db 528 ASIIEGPGFTGGLNLFKESNSIAKFVTLNSAALLQRYVRIRVAST-----TNLRL 581

Qy 632 TIPGVIGIPQRLNNTFSGTNYN-----NLQYGDGYFPQFPSTVTLPLNRNPIFNR 684

Db 582 FV-----QNSNDFLVIYINKTMKDDLTQYTFDLATTNSNMFGSKDKNELIIGAE 633

Qy 685 ADVNSNLIIDKIEFPI 702

Db 634 SFVSNKIIYIDKIEFIPV 651

RESULT 13

US-11-192-801-16

; Sequence 16, Application US/11192801

; Publication No. US20050273882A1

; GENERAL INFORMATION:

; APPLICANT: Romano, Charles P.

; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

; CURRENT APPLICATION NUMBER: US/11/192,801

; PRIOR FILING DATE: 2005-07-29

; PRIOR APPLICATION NUMBER: US/10/232,665

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US/09/377,466

; PRIOR FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16



Db 634 SFVSNKIEYIDKIEFIPV 651

RESULT 15

US-11-192-801-20

; Sequence 20, Application US/11192801

; Publication No. US20050273882A1

; GENERAL INFORMATION:

; APPLICANT: Ronano, Charles P.

; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

; CURRENT APPLICATION NUMBER: US/11/192,801

; CURRENT FILING DATE: 2005-07-29

; PRIOR APPLICATION NUMBER: US/10/232,665

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US/09/377,466

; PRIOR FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 653

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: PRT

; LOCATION: (1)..(653)

; OTHER INFORMATION: Cry3Bb1 variant 11231mv1

US-11-192-801-20

Query Match 17.5%; Score 683; DB 7; Length 653;

Best Local Similarity 28.0%; Pred. No. 4.9e-44;

Matches 207; Conservative 122; Mismatches 283; Indels 126; Gaps 28;

QY 2 NQNNNEYEILDSKNSLSPNSRNIDHSRYPYTNPNQPLONTNYKWLNMCO-GNTQYGD 60

Db 3 NPNNRSEHDTI---KVTNPNSELQTNQYPLADPNSTLEELNYKBFRLMTEDSSTSEVL 59

QY 61 NPETPASADTIA-AVSAGTIVSGTLGAGLGLTSISGPIGIIAGIIISFGTLITVFWPAG 119

Db 60 N-----STVKDVGTVGIVGQILGVGV-----VFFAGALTSFYQSFLNTIWPSS- 103

QY 120 EQDKTVMTQFIKMGEIFVDPPTLPTESIKQLKLOTLEGFRQILQSYNTALDDWRKLRLOAP 179

Db 104 --DADPWKAFMAQVEVLIDKKBEEYAKSALAELQGLQNNFEDYVNALNSWKK----- 154

QY 180 GLPPSSALQQAALTILKIRFENVNDIFRIPGQLETYKTLPIPIYAQAANFHLNLLQOG 239

Db 155 -TPLSLRSKRSGRIRRELFSAESHFRNMGMPSPAVSKFEVLFLPTYAQAANTHLLLLKDA 213

QY 240 AELADEWNADIHPSQIEPNAGTSDD--VYKLLKENIPKYSNYCANTYREGNKLKRNENP 296

Db 214 QVFGEEWGY-----SSEDVAEFRRQLKLTQQTTHCVNWNVGNLGRGSTY 261

QY 297 MRWSIFNDYRRYMTITVLDTIAQFSYDIKRYKDSIGRIGGKTELTRITTYTEINFDR 356

Db 262 DAWVKFNRRFRREMTLVLDLIVLFPFYDIRLYSK-----GVKTELTRIDFTDPI-FLLT 314

QY 357 TYLEIOPNLAIMYNTIRSGRLRFLSFDELIFYTK-----NETYGNRLVGIANR 405

Db 315 TLQYGTPTFLSIENSIRKP--HLFDYLOQIEFHTLRPGYFGKDSFNYWSGNY---VETR 369

QY 406 NRSTYATTGTIELIYGERTGPTTKTLIPESYKSVITDRQV--TPTSPPFN--IYFTIN 461

Db 370 PSIGSSKTITSPYQKSTPEVOK--LSFDGQKYV-----RTANTDVAAWPNKGKYLGV 423

QY 462 QIELYLNNSPSNKL-----TYSA---GGNLSNDKKTDFQFPVKDKCKPIINPNCLPSYNS 515

Db 424 KVDFSQYDDQKNETSQTQYDSKRNNGHVSQAQDSID--QLPPTTDEPL-----EKAY 473

QY 516 SHILSOFSLPNYSYKIGLALNIIYTGALGWTSHSVNRNNAISDKIITMIPAIKGNSLDTN 575

Db 474 SHQNTYAECFLMQDRRGTI--PFFT-----WTHRSVDFFNTIDAEKITQLFPVKAYALSSG 527

QY 576 SKVIEGPGHTGNNLVYLO-----SQRLEITCTPNSQSYIIRLRVATNGAGNTLPNISL 631

Db 528 ASIIIEGPGFTGNNLLFLKSSNSIAKFKVTLNSAALLQRYRVIRYAST-----TNLRL 581

QY 632 TIPGVIGIPPPQRLNNTFSGTNYN-----NIQYGDGFGYFQFPSTVTLPLNRNIPFIPNR 684

Db 582 FV-----QNSNNDFLVIYINKTMKODDLTYQTDFDLATTNSNMFGSGDKNELIIGAB 633

QY 685 ADVSNSILLIIDKIEFPI 702

Db 634 SFVSNKIEYIDKIEFIPV 651

Search completed: December 15, 2005, 10:59:54

Job time : 18 secs



GenCoré version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:34:42 ; Search time 189 Seconds  
(without alignments)  
1729.618 Million cell updates/sec

Title: US-10-782-570-2

Perfect score: 3906

Sequence: 1 MNQNNNEVEIIDSKNLSYP.....FFTNHTKNTLNIEATNYDID 744

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004as.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3906	100.0	744	8	ADR89397
2	3623	92.8	694	8	ADR89399
3	3318	84.9	735	8	ADR89395
4	1159	29.7	1180	1	RAP93715
5	1158	29.6	1180	8	ADR89426
6	1157	29.6	1016	1	RAP94035
7	1157	29.6	1180	1	RAP82589
8	1153	29.5	1180	2	AAR14373
9	1153	29.5	1180	2	AAR63078
10	901	23.1	1109	5	RAE26353
11	901	23.1	1109	7	ADF31302
12	901	23.1	1109	7	ADF31307
13	900	23.0	686	2	RAR63079
14	899	23.0	675	2	AAR14374
15	897	23.0	675	8	ADR89431
16	897	23.0	675	9	ADY59866
17	819	21.0	1136	5	AAU76029
18	819	21.0	1136	8	ADR89427
19	819	21.0	1136	9	AEA61391
20	818	20.9	1136	1	RAP93341
21	816	20.9	1136	1	RAP82314
22	791.5	20.3	1169	2	AAW06417
23	772.5	19.8	1095	1	AAP97052
24	755	19.3	1178	1	RAP60051

25	720	18.4	1210	5	AAU99256
26	720	18.4	1210	8	ADL15307
27	720	18.4	1210	9	AEb45609
28	712.5	18.2	780	9	AEA81472
29	712.5	18.2	1169	9	AEA81468
30	710	18.2	651	2	AAW06460
31	710	18.2	651	2	AAW06419
32	710	18.2	659	2	AAW23213
33	710	18.2	659	8	ADR89424
34	709.5	18.2	682	8	ADR89433
35	704	18.0	652	2	AAW23211
36	704	18.0	652	3	AAW70442
37	704	18.0	652	6	ABU09193
38	704	18.0	652	7	ABW01051
39	703	18.0	1206	5	AAU99255
40	703	18.0	1206	8	ADL15305
41	703	18.0	1206	9	AEb45607
42	699	17.9	651	2	RAR33769
43	697	17.8	652	3	AAW70443
44	697	17.8	652	6	ABU09194
45	697	17.8	652	7	ABW01052

#### ALIGNMENTS

RESULT 1	
ADR89397	
ID	ADR89397 standard; protein; 744 AA.
XX	
AC	ADR89397;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	AXMI-007.
XX	
KW	delta-endotoxin; delta-endotoxin associate polypeptide;
KW	expression cassette; transformation; transgenic; plant; bacteria;
KW	lepidoptera; coleoptera; pest; pesticide; resistance;
KW	pesticidal activity.
XX	
OS	Bacillus thuringiensis.
XX	
XX	
Key	Location/Qualifiers
FT	Key
FT	Misc-difference 1
FT	/note= "encoded by GTG"
XX	
XX	WO2004074462-A2.
XX	
PD	02-SEP-2004.
XX	
XX	20-FEB-2004; 2004WO-US005829.
XX	
PR	20-FEB-2003; 2003US-0448632P.
PR	20-FEB-2003; 2003US-0448633P.
PR	20-FEB-2003; 2003US-0448797P.
PR	20-FEB-2003; 2003US-0448806P.
PR	20-FEB-2003; 2003US-0448810P.
PR	20-FEB-2003; 2003US-0448812P.
PR	19-FEB-2004; 2004US-00781979.
PR	19-FEB-2004; 2004US-00782020.
PR	19-FEB-2004; 2004US-00782096.
PR	19-FEB-2004; 2004US-00782141.
PR	19-FEB-2004; 2004US-00782570.
PR	19-FEB-2004; 2004US-00783417.
XX	
XX	(ATHE-) ATHENIX CORP.
PA	
XX	
PI	Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX	
DR	WPI; 2004-635574/61.
DR	N-PSDB; ADR89396.
XX	

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
 PT for producing organisms with pesticide resistance.

XX Claim 12; SEQ ID NO 9; 178pp; English.

PS This sequence represents an isolated delta-endotoxin. Some of the delta-  
 XX endotoxin coding sequences of the invention have alternative start  
 CC codons, producing more than one protein from a single open reading frame.  
 CC The nucleic acid sequences of the invention are useful in DNA constructs  
 CC or expression cassettes for transformation and expression in plants and  
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
 CC killing lepidopteran or coleopteran pests. Compositions containing the  
 CC delta-endotoxins of the invention, and methods for their production, are  
 CC useful for the production of organisms with pesticide resistance,  
 CC specifically bacteria and plants. These organisms are useful for  
 CC generating altered or improved delta-endotoxin or delta-endotoxin-  
 CC associated proteins that have pesticidal activity, or for detecting the  
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
 CC nucleic acids in products or organisms.

XX Sequence 744 AA;

Query Match 100.0%; Score 3906; DB 8; Length 744;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-304;  
 Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQNNNEYEIIIDSKNLSYSPNRNIDHSRYPTNNPNQPLQNTNYKWLNNCQNTQYGD 60  
 DB 1 MNQNNNEYEIIIDSKNLSYSPNRNIDHSRYPTNNPNQPLQNTNYKWLNNCQNTQYGD 60  
 QY 61 NFEFASADTIAVSAAGTIVSGTLLAGIGGTSISGPIIGIIGIISFGTLITVFPAGE 120  
 DB 61 NFEFASADTIAVSAAGTIVSGTLLAGIGGTSISGPIIGIIGIISFGTLITVFPAGE 120  
 QY 121 QDKTVMTQFIMGEIFVDVPLTESIKQLQTLLEGFRQILQSYNTALDDMRKRLQAPG 180  
 DB 121 QDKTVMTQFIMGEIFVDVPLTESIKQLQTLLEGFRQILQSYNTALDDMRKRLQAPG 180  
 QY 181 LPSSALQQAALTILKIFENVHNDPREIFGFOLEYKTLPIYQAANFHLNLQOGA 240  
 DB 181 LPSSALQQAALTILKIFENVHNDPREIFGFOLEYKTLPIYQAANFHLNLQOGA 240  
 QY 241 ELADEWNADTHPSQIEBNAQSDYYKLLKENIPKYSNCANTYREGNKLKRNPNRWS 300  
 DB 241 ELADEWNADTHPSQIEBNAQSDYYKLLKENIPKYSNCANTYREGNKLKRNPNRWS 300  
 QY 301 IFNDYRYMTITVLDITIAQSFYDIKRYKDSIGRIGGIKTELTRREIYTTTEINFDRLTLE 360  
 DB 301 IFNDYRYMTITVLDITIAQSFYDIKRYKDSIGRIGGIKTELTRREIYTTTEINFDRLTLE 360  
 QY 361 IQPNLAIMEYNLRSGURLFSFLDELIFYTNYETGNRLVGIANRNRSTVATTGTEIYG 420  
 DB 361 IQPNLAIMEYNLRSGURLFSFLDELIFYTNYETGNRLVGIANRNRSTVATTGTEIYG 420  
 QY 421 ERTGPPTTKLIPESYKVSIVTDQVTPSPNNIYFTINQELYNLSPSKNLTVSAG 480  
 DB 421 ERTGPPTTKLIPESYKVSIVTDQVTPSPNNIYFTINQELYNLSPSKNLTVSAG 480  
 QY 481 GNLSDNKKTTDFQPPVKCKPIINPNCLPSYNSHILSQSFLFNYSYKIGLALNLYT 540  
 DB 481 GNLSDNKKTTDFQPPVKCKPIINPNCLPSYNSHILSQSFLFNYSYKIGLALNLYT 540  
 QY 541 GALTGHTSSVNRNNAISDKIITMIPAKGNLSLDTNSKVIEGPGHGTGNLVYLSQGRLEI 600  
 DB 541 GALTGHTSSVNRNNAISDKIITMIPAKGNLSLDTNSKVIEGPGHGTGNLVYLSQGRLEI 600  
 QY 601 TCRTPNSTQSYIRLRVATNGAGNLTENISLTIPGVIGIPPPRLNNTFSGTNNYNNLYQGD 660  
 DB 601 TCRTPNSTQSYIRLRVATNGAGNLTENISLTIPGVIGIPPPRLNNTFSGTNNYNNLYQGD 660  
 QY 661 FGYPFPSTVTLPLNRNPIFNRAVDSNLSILIDKIEFIPITSSVRQNRKQKLETIQT 720  
 DB 661 FGYPFPSTVTLPLNRNPIFNRAVDSNLSILIDKIEFIPITSSVRQNRKQKLETIQT 720

DB 661 FGYPFPSTVTLPLNRNPIFNRAVDSNLSILIDKIEFIPITSSVRQNRKQKLETIQT 720  
 QY 721 KINTFFTNHTKNTLNIEATNYDID 744  
 DB 721 KINTFFTNHTKNTLNIEATNYDID 744

RESULT 2  
 ADR89399

ID ADR89399 standard; protein; 694 AA.

XX ADR89399;

DT 18-NOV-2004 (first entry)

DE AXMI-007 alternative protein.

XX delta-endotoxin; delta-endotoxin associate polypeptide;  
 KW expression cassette; transformation; transgenic; plant; bacteria;  
 KW lepidoptera; coleoptera; pest; pesticide; resistance;  
 KW pesticidal activity.

XX Bacillus thuringiensis.

XX WO2004074462-A2.

XX 02-SEP-2004.

XX 20-FEB-2004; 2004WO-US005829.

XX 20-FEB-2003; 2003US-0448632P.

XX 20-FEB-2003; 2003US-0448633P.

XX 20-FEB-2003; 2003US-0448797P.

XX 20-FEB-2003; 2003US-0448806P.

XX 20-FEB-2003; 2003US-0448810P.

XX 19-FEB-2003; 2003US-0448812P.

XX 19-FEB-2004; 2004US-00781979.

XX 19-FEB-2004; 2004US-00782020.

XX 19-FEB-2004; 2004US-00782096.

XX 19-FEB-2004; 2004US-00782141.

XX 19-FEB-2004; 2004US-00782570.

XX 19-FEB-2004; 2004US-00783417.

XX (ATHE-) ATHENIX CORP.

XX Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;

XX WPI; 2004-635574/61.

XX N-PSDB; ADR89398.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
 PT for producing organisms with pesticide resistance.

XX Claim 12; SEQ ID NO 11; 178pp; English.

XX This sequence represents an isolated delta-endotoxin. Some of the delta-  
 CC endotoxin coding sequences of the invention have alternative start  
 CC codons, producing more than one protein from a single open reading frame.  
 CC The nucleic acid sequences of the invention are useful in DNA constructs  
 CC or expression cassettes for transformation and expression in plants and  
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
 CC killing lepidopteran or coleopteran pests. Compositions containing the  
 CC delta-endotoxins of the invention, and methods for their production, are  
 CC useful for the production of organisms with pesticide resistance,  
 CC specifically bacteria and plants. These organisms are useful for  
 CC generating altered or improved delta-endotoxin or delta-endotoxin-  
 CC associated proteins that have pesticidal activity, or for detecting the  
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
 CC nucleic acids in products or organisms.

XX Sequence 694 AA;

Query Match		92.8%; Score 3623; DB 8; Length 694;
Best Local Similarity		100.0%; Pred. No. 8e-282;
Matches 694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	51	MCQNTQYGDNFETPASADTTAAVSAGTIVSGTLLAGIGGLTSISGPIIGIIGAIISFGT 110
Db	1	MCQNTQYGDNFETPASADTTAAVSAGTIVSGTLLAGIGGLTSISGPIIGIIGAIISFGT 60
Qy	111	LITVFWPAGEODKVTWTFQIKWGEIFVDTPTESIKQLKLTLEGFRQILQSYNTALDDW 170
Db	61	LITVFWPAGEODKVTWTFQIKWGEIFVDTPTESIKQLKLTLEGFRQILQSYNTALDDW 120
Qy	171	RKLKLOAPGLPPSALQQAALTILKIRPENVHNDPIREIFGQLETKYKTLTLLPIYAQAN 230
Db	121	RKLKLOAPGLPPSALQQAALTILKIRPENVHNDPIREIFGQLETKYKTLTLLPIYAQAN 180
Qy	231	PHNLLQQAELADENADHPSQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGLNK 290
Db	181	PHNLLQQAELADENADHPSQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGLNK 240
Qy	291	LRNEPNRWSIFNDYRRYMTITVLDTIAQFSFYDIKRYKDSIGRIGGKTELTREIYTT 350
Db	241	LRNEPNRWSIFNDYRRYMTITVLDTIAQFSFYDIKRYKDSIGRIGGKTELTREIYTT 300
Qy	351	INFRLTYLEIQPNLAIMEYNLTSGRLPFLDELIFYTKNETYGNRLVGIANRSTY 410
Db	301	INFRLTYLEIQPNLAIMEYNLTSGRLPFLDELIFYTKNETYGNRLVGIANRSTY 360
Qy	411	ATTGTEIYIGERTGPTTKTILIPESYKSVITVDQVTPSPFPNIYFTINOIELYLNS 470
Db	361	ATTGTEIYIGERTGPTTKTILIPESYKSVITVDQVTPSPFPNIYFTINOIELYLNS 420
Qy	471	PSNKLTYSAGNLSNDKTTDFQFPVKCKDCKPIINPNCLPSYNSYSHLSFSLFNYSYK 530
Db	421	PSNKLTYSAGNLSNDKTTDFQFPVKCKDCKPIINPNCLPSYNSYSHLSFSLFNYSYK 480
Qy	531	IGLALNLYTGALGWTSSVNRNNAISDKIITMIPAIKNSLDTSKSVIEGPGHTGNLV 590
Db	481	IGLALNLYTGALGWTSSVNRNNAISDKIITMIPAIKNSLDTSKSVIEGPGHTGNLV 540
Qy	591	YLOSQRLTCTRPNSTQSYIIRLYATGAGNTLPNISITIPGVIGIPORLNNTPSG 650
Db	541	YLOSQRLTCTRPNSTQSYIIRLYATGAGNTLPNISITIPGVIGIPORLNNTPSG 600
Qy	651	TNYNLQYDGFYQFPFTVTLPLNRNIPFIFNRADVSNLSIILDKIEFIPITSSVRQNR 710
Db	601	TNYNLQYDGFYQFPFTVTLPLNRNIPFIFNRADVSNLSIILDKIEFIPITSSVRQNR 660
Qy	711	EKQKLETIQKINTFFTNHTKNTLNIEATNYDID 744
Db	661	EKQKLETIQKINTFFTNHTKNTLNIEATNYDID 694
RESULT 3		
ID	ADR89395	standard; protein; 735 AA.
XX	AC	ADR89395;
XX	AC	ADR89395;
DT	18-NOV-2004	(first entry)
XX	DE	AXMI-006.
XX	KW	delta-endotoxin; delta-endotoxin associate polypeptide;
KW	KW	expression cassette; transformation; transgenic; plant; bacteria;
KW	KW	lepidoptera; coleoptera; pest; pesticide; resistance;
XX	OS	pesticidal activity.
XX	OS	Bacillus thuringiensis.
PN	W02004074462-A2.	
XX	PD	02-SEP-2004.

XX 20-FEB-2004; 2004WO-US005829.  
 XX 20-FEB-2003; 2003US-0448632P.  
 PR 20-FEB-2003; 2003US-0448632P.  
 PR 20-FEB-2003; 2003US-0448797P.  
 PR 20-FEB-2003; 2003US-0448806P.  
 PR 20-FEB-2003; 2003US-0448810P.  
 PR 20-FEB-2003; 2003US-0448812P.  
 PR 19-FEB-2004; 2004US-00781979.  
 PR 19-FEB-2004; 2004US-00782020.  
 PR 19-FEB-2004; 2004US-00782096.  
 PR 19-FEB-2004; 2004US-00782141.  
 PR 19-FEB-2004; 2004US-00782570.  
 PR 19-FEB-2004; 2004US-00783417.  
 XX (ATHE-) ATHENIX CORP.  
 XX Carozzi N, Hargiss T, Koziele MG, Duck NB, Carr B;  
 WPI; 2004-635574/61.  
 N-PSDB; ADR89394.

New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.

Claim 12; SEQ ID NO 7; 178pp; English.

This sequence represents an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

Sequence 735 AA;

Query Match 84.9%; Score 3318; DB 8; Length 735;  
 Best Local Similarity 87.1%; Pred. No. 2.9e-257;  
 Matches 639; Conservative 31; Mismatches 60; Indels 4; Gaps 3;

Qy 1 MNQNN-NNEYEIIIDSKNLSYPNSNRNIDHSYPYTNPNQPLONTNYKEWLNMCQNTQY 59  
 Db 1 MNQNN-NNEYEIIIDSKNLSYPYFPNNSNDSRYPTNNPNQPLONTNYKEWLNMCQNTQY 60  
 Qy 60 DNFETPASADTTAAVSAGTIVSGTLLAGIGGLTSISGPIIGIIGAIISFGTITVFWPAG 119  
 Db 61 DNFETPASADTTAAVSAGTIVSGTLLAGIGGLTSISGPIIGIIGAIISFGTITVFWPAG 120  
 Qy 120 EODKTVMTQIKWGEIFVDTPTESIKQLKLTLEGFRQILQSYNTALDDWRKLRLOAP 179  
 Db 121 EODKTVMTQIKWGEIFVDTPTESIKQLKLTLEGFRQILQSYNTALDDWRKLRLOAP 180  
 Qy 180 GLPPSSALQQAALTILKIRPENVHNDPIREIFGQLETKYKTLTLLPIYAQANFHLNLQOG 239  
 Db 181 GLPPSSALQQAALTILKIRPENVHNDPIREIFGQLETKYKTLTLLPIYAQANFHLNLQOG 240  
 Qy 240 AELADEWNADHPSQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGLNKLRNEPNRW 299  
 Db 241 AELADEWNADHPSQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGLNKLRNEPNRW 300  
 Qy 300 SIFNDYRRYMTITVLDTIAQFSFYDIKRYKDSIG--RIGGIKTELTREIYTTINFORLT 357  
 Db 301 SIFNDYRRYMTITVLDTISQFSLYDIKRYDSIGGIEVKIGIKNELTREIYTTINFORLP 360



pesticidal activity.

Bacillus thuringiensis.

WO2004074462-A2.

02-SEP-2004.

20-FEB-2004; 2004WO-US005829.

20-FEB-2003; 2003US-0448632P.

20-FEB-2003; 2003US-0448633P.

20-FEB-2003; 2003US-0448797P.

20-FEB-2003; 2003US-0448806P.

20-FEB-2003; 2003US-0448810P.

20-FEB-2003; 2003US-0448812P.

19-FEB-2004; 2004US-00781979.

19-FEB-2004; 2004US-00782020.

19-FEB-2004; 2004US-00782096.

19-FEB-2004; 2004US-00782141.

19-FEB-2004; 2004US-00782570.

19-FEB-2004; 2004US-00783417.

(ATHE-) ATHENIX CORP.

Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

WPI, 2004-635574/61.

New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.

Example 6; SEQ ID NO 38; 178pp; English.

This sequence represents a delta-endotoxin crystal protein. This protein was included in the scope of the invention as a comparison to the delta-endotoxins of the invention. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

Sequence 1180 AA;

Query Match 29.6%; Score 1158; DB 8; Length 1180;

Best Local Similarity 37.3%; Pred. No. 2.8e-83;

Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;

QY 5 NNNVEYIIDS--KNLSYPSNENIDHSYPTNNPNOPLQNTNYKEWLMCOGNTQYGDNF 62

DB 6 NKNYEYTLNASQKCLNLSNN---YTRYPIENSFKQLQSTNYKDLNLMCOQNOYGGDF 61

QY 63 ETFASADTIAAVSAGTIVSGTLGAGLTSISGPIGIIAISFGTLITVFWPAGEQD 122

DB 62 ETFIDS---GELSYATIVGVILGFGFTT---PLGL---ALIGFTLIPVLPFAQDS 111

QY 123 KTVMTQIKMGEIFVDPTLIESIKQLKQTLLEGFRQILQSYNTALDWRKLRQAQGLP 182

DB 112 NT-MSDFITQTKIIEASTYISNANKILNRSFNVIYSTVHNHKTWE-----NNENPQ 165

QY 183 PSSALQAALTLKTRFENVHDFREIP--GFQLETYKTLILPIYAAANPHLNLQOGA 240

DB 166 NTQDVRTQIQLVHVHFQNVPELVNSCFPNPSCDYNILVLSYAAANLHLTVLNOAV 225

241 ELADENWADIHPSQI EPNACTSDDYKYLKAKENTIPKYSNYCANTYREGINKLRNBP----- 295

226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTKAIEDYTNVCVTYTKGGLNLIKTTDPDNL 284

296 -NMRWSIFNDYRRYMTITVLDTTAQSFYDKYKDSIGRIGGKTKLTREIYITTEINPD 354

285 GNINMNTYNTYRTKMTTAVLDLVALFPNYDVGYPI-----GVQSELTREIYQV-LNFE 337

355 RLTYLEIQPNLAIMEVNLTRSLRFLSFDELFIYTKNRYGRLVGIANRRSTYA--- 411

338 ESPYKY--DFQVEDSLTERP-HLFTWLDLSLNFYKAOITPNNFF-TSHYNMFHYTLDN 393

412 TTGTEIYGBRTGPTTKTLIPESYKVSIVTRQVTPTPSPFNPIYFTINOIELYLNNSP 471

394 ISQKSSVFGNHNVTDLKLSL--GLATNIYIFLLNVLISLDNKYLDVNNISKMDPFFITNGT 451

472 ---SNKLTYSAGGLNSNDKTTDFQPVKDCPKIINPNCPLPSVNSYSHILSQSFLNY- 527

452 RLLEKELT-AGSGQITVDVNNKIFGLPKRRENGQNTLFPYTDVNSYSHILSPKLSUP 510

528 -SYKIGLALNLYTGALGTHSSVNRNNAISDKIITMIPAIGNSLDTNSKVIEGPGHTG 586

511 ATYK-----TQVTFPA--WTHSSVDPKNTIYTHLTQIPAVKANSLGTASKVQGPHTG 563

587 GNLVYLSQGRLEITCRTPNSTQSYIIRLYATNGAGNTLPLNISLTIPGVIGIPPPRLNN 646

564 GDLI--DFKDHFKITCQHSNFQSYFIRIYASNGSANTRAVINLSIPGVAEL-GMALNP 620

647 TFGSTNNLYQDGFYGFQFPSTVTPLNRIPIFNRAVY-NSNILLIDKIEPIPTSS 705

621 TFGSTDTNLYKDFQYLFESNEVKFAPNQNISLVFNRSVDYTNNTVLDIKIEFLPITRS 680

706 VRONREKQKLETTQKINTFEFTNHTKNTLNIEATNYDID 744

681 IREDREKQKLETTQKINTFEFTNHTKNTLNIEATNYDID 719

RESULT 6

AAP94035

ID AAP94035 standard; protein; 1016 AA.

AC AAP94035;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 30-MAY-1990 (first entry)

XX Delta-endotoxin crystal protein.

DE Delta-endotoxin; crystal protein; insecticide; pCC130;

XX biological control agent.

XX Bacillus thuringiensis; israelensis.

XX RP296870-A.

XX 28-DEC-1988.

XX 24-JUN-1988; 88EP-00305772.

XX 26-JUN-1987; 87US-00067653.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Eilar DJ, Ward ES;

XX WPI; 1989-001322/01.

XX N-PSDB; AAN93054.

XX DNA fragment encoding insecticidal protein - obt'd. from Bacillus thuringiensis sub species israelensis, and used in microorganisms and plant cells.









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Query Match      23.1%; Score 901; DB 5; Length 1109;
Best Local Similarity 34.2%; Pred. No. 1.2e-62;
Matches 240; Conservative 106; Mismatches 242; Indels 114; Gaps 27;

QY 67 SADTIAAVSAGTIVSGTLLAGIGLTSIGPIGIIIGAIISFGTLITVFWPAGQD-KTV 125
DB 28 SSDTAVVVSAGIVVVGITLT---AFASFVNP---GVVLISFGTLAPVLPDPBEDPKKI 80
QY 126 WTQIKMGEIFVDVPLTESIKQLKLTLEGFRQLQSNTALDWRKLRLOAQGLPPSS 185
DB 81 WSQFMKGEDLLNQITISAVKIALAHNGFKDVLTYTTERAFNDWKR-----NPSA 131
QY 186 ALQQAALTLKTRFENVHDFIREIPGFOLEYTKLLLPYAAQAAFNHLNLQOAGLADE 245
DB 132 ---NTARLVSRQFENAHFNVSNPQLQPTDYLTLSSCYTEAANHLNLHOGVQFADQ 188
QY 246 WNADHPSQIEPNAGTSDDYKLLKENIPKYSNVCANTYREGKLNKRNPNRWSIFNDY 305
DB 189 WNADQPHSPMLKSSGT---YYDELLVYIEKYINCTKYHGLNHLKSEKITTWDYNTY 245
QY 306 RRYMTITVLTIAOFSFYDIKRYKDSIGRIGIKTELTREIYTTINFDRLTYLEIOPNL 365
DB 246 RREMTLIVDLVATFPFYDIRFP-----RGVELELTREYVTS-----LDHLTRPPG- 292
QY 366 AIMEYNLTRSGRLRFSFDELIFYTKNETYGNRLVIGIANRNRSTVATGTETI-----IYG 420
DB 293 -----LFTWLSDIELYTESVAEGDYLSGI-----RESKYTYGNQFTWKNIYG 335
QY 421 ERTGPPTTK-----TLIPFESYKVSIVTDQVTPFPFNIIYFTINOIELYLNNSPNK 474
DB 336 N-----TNRLSKQLITLLPGE-FWTHLSINRPPQTIAGINKLYSLIQKI-----VFTFKND 386
QY 530 KIGLALNLTGALGTHSSVNRNNAISDKIITMIPAIKGNSLDTSNKVIEGPGHTGNL 589
DB 434 EFAEYFHSIF--ALGWTNHSVNSQNLISESVSTQIPLVKADEV-TNNSVIRGPGTGGDL 490
QY 590 VYLOSQRLEITCRTPNSTQSYIIRLVATNGAGNTLPNLSLTIPGVIGIPQRLNWTFS 649
DB 491 IELRD--KCSIKCKA--SSLKYYAISLFYAANNAIVSIVDGDGAGVL-----LQPTFS 541
QY 650 GTNVNN-----LOYDGFYGFQFPSTVTLPLNRNIPFIFNRAD--VNSILIIDKIEFPI 702
DB 542 RKGNNFTIQDLNFKDYHLLVDIELPESEEHHLKREDDYEEGVILLIDKLEFKPI 601
QY 703 TSSVRQNRKQKLEITQIKNTFFTNHTKNTLNIEATNYDID 744
DB 602 DENY---TNEMNLEKAKKAVNVLFINAT-NALKMDVTDYHID 639

RESULT 11
ADF31302
ID ADF31302 standard, protein; 1109 AA.
XX AC ADF311302;
XX AC ADF311302;
XX DT 12-FEB-2004 (first entry)
XX DE Bacillus thuringiensis serovar finitimus cry28Aa1 delta-endotoxin.
XX KW Cry28Aa1; delta-endotoxin; insect pest control;
XX KW transgenic plant; insect resistance; insecticide.
XX OS Bacillus thuringiensis serovar finitimus.
XX PN US2003150018-A1.
XX PD 07-AUG-2003.
XX PF 15-JAN-2003; 2003US-00345020.

XX 07-JAN-2000; 2000US-0175158P.
PR 08-JAN-2001; 2001US-00756526.
XX (WOJC/) WOJCIECHOWSKA J A.
PA (LEWI/) LEWITIN E I.
PA (ZALU/) ZALUNIN I A.
PA (REVI/) REVINA L P.
PA (CHES/) CHESTUKHINA G G.
PI Wojciechowska JA, Lewitin EI, Zalunin IA, Revina LP;
PI Chestukhina GG;
XX WI; 2003-897623/82.
DR N-PSDB; ADF31301.
XX New isolated nucleic acid molecule encoding a toxin that is active
PT against insects useful for controlling insect pests or for conferring
PT insect resistance in plants.
XX Claim 22; SEQ ID NO 4; 42pp; English.
XX The present invention relates to the isolation of novel cry26Aa1 and
CC cry28Aa1 delta-endotoxin genes from Bacillus thuringiensis ssp.
CC finitimus. The sequences for the delta-endotoxin polypeptides are also
CC disclosed. The invention provides methods for producing the toxins and
CC compositions containing the toxins. The methods and sequences of the
CC invention are useful for controlling insect pests in transgenic plants to
CC confer insect resistance. The present sequence represents the cry28Aa1
CC delta-endotoxin of the invention.
XX Sequence 1109 AA;
XX Query Match      23.1%; Score 901; DB 7; Length 1109;
XX Best Local Similarity 34.2%; Pred. No. 1.2e-62;
XX Matches 240; Conservative 106; Mismatches 242; Indels 114; Gaps 27;
QY 67 SADTIAAVSAGTIVSGTLLAGIGLTSIGPIGIIIGAIISFGTLITVFWPAGQD-KTV 125
DB 28 SSDTAVVVSAGIVVVGITLT---AFASFVNP---GVVLISFGTLAPVLPDPBEDPKKI 80
QY 126 WTQIKMGEIFVDVPLTESIKQLKLTLEGFRQLQSNTALDWRKLRLOAQGLPPSS 185
DB 81 WSQFMKGEDLLNQITISAVKIALAHNGFKDVLTYTTERAFNDWKR-----NPSA 131
QY 186 ALQQAALTLKTRFENVHDFIREIPGFOLEYTKLLLPYAAQAAFNHLNLQOAGLADE 245
DB 132 ---NTARLVSRQFENAHFNVSNPQLQPTDYLTLSSCYTEAANHLNLHOGVQFADQ 188
QY 246 WNADHPSQIEPNAGTSDDYKLLKENIPKYSNVCANTYREGKLNKRNPNRWSIFNDY 305
DB 189 WNADQPHSPMLKSSGT---YYDELLVYIEKYINCTKYHGLNHLKSEKITTWDYNTY 245
QY 306 RRYMTITVLTIAOFSFYDIKRYKDSIGRIGIKTELTREIYTTINFDRLTYLEIOPNL 365
DB 246 RREMTLIVDLVATFPFYDIRFP-----RGVELELTREYVTS-----LDHLTRPPG- 292
QY 366 AIMEYNLTRSGRLRFSFDELIFYTKNETYGNRLVIGIANRNRSTVATGTETI-----IYG 420
DB 293 -----LFTWLSDIELYTESVAEGDYLSGI-----RESKYTYGNQFTWKNIYG 335
QY 421 ERTGPPTTK-----TLIPFESYKVSIVTDQVTPFPFNIIYFTINOIELYLNNSPNK 474
DB 336 N-----TNRLSKQLITLLPGE-FWTHLSINRPPQTIAGINKLYSLIQKI-----VFTFKND 386
QY 530 KIGLALNLTGALGTHSSVNRNNAISDKIITMIPAIKGNSLDTSNKVIEGPGHTGNL 589
DB 434 EFAEYFHSIF--ALGWTNHSVNSQNLISESVSTQIPLVKADEV-TNNSVIRGPGTGGDL 490
QY 590 VYLOSQRLEITCRTPNSTQSYIIRLVATNGAGNTLPNLSLTIPGVIGIPQRLNWTFS 649
DB 491 IELRD--KCSIKCKA--SSLKYYAISLFYAANNAIVSIVDGDGAGVL-----LQPTFS 541
QY 650 GTNVNN-----LOYDGFYGFQFPSTVTLPLNRNIPFIFNRAD--VNSILIIDKIEFPI 702
DB 542 RKGNNFTIQDLNFKDYHLLVDIELPESEEHHLKREDDYEEGVILLIDKLEFKPI 601
QY 703 TSSVRQNRKQKLEITQIKNTFFTNHTKNTLNIEATNYDID 744
DB 602 DENY---TNEMNLEKAKKAVNVLFINAT-NALKMDVTDYHID 639
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XX WPI; 1995-067338/09.
DR N-PSDB; AAQ81180.
XX Method for controlling Calliphoridae pests - specifically utilises
XX Bacillus thuringiensis isolates or toxins.
XX Disclosure; Page 42-43; 50pp; English.
XX A library was constructed from Bacillus thuringiensis PS71M3 total
XX cellular DNA in lambda Gem-11. Plasmid pMVC1636, selected in Escherichia
XX coli, contained a 15 kb insert expressing a beta-endotoxin gene. This was
XX sequenced (AAQ81180). A cured, acrycstalliferous B.t. host carrying
XX pMVC1636 produced a 77 kDa crystal protein (AAR63079). (Updated on 25-MAR
XX -2003 to correct PN field.)
XX Sequence 686 AA;

Query Match      23.0%; Score 900; DB 2; Length 686;
Best Local Similarity 32.9%; Pred. No. 6.8e-63;
Matches 251; Conservative 115; Mismatches 268; Indels 128; Gaps 32;

Qy 5 NNNVEYIIDSKNLSYPSNRNIDHSRYPTNNPNQPLQNTNYKEWLNMCQGNTOYQDNFET 64
Db 6 NKNEYEIFNAPSNNGFSKNN--YSRYPLANKPNQPLKNTNYKQWLNVCQDNQOQYGNNA 63
Qy 65 PASADTTAAVSAGTIIVSGTLTLAGIGLTSISGPIIGIICAIISFGTLITVFWPAGEQDKT 124
Db 64 FVSSETIVGSAGIIVVGTMLG-----AFAAP--VLAAGIISFGTLPIFW-QGSDPAN 114
Qy 125 VWTQFIKMGEIFVDTPLTE---SIKQLKLTLEGFROILOSNTALDDWRKLEQAPGL 181
Db 115 VWQDLLNIG---GRPIQIEDKNIINVLTSIVTPIKNQLDKYQEFFDKWEPAR----- 163
Qy 182 PPSALQQAALTUKIRENVHN---DFIREIPGQLETYKTLPIYAQAANFHLNLLQ 238
Db 164 --THANAKAVHDLFTTLEPIIDKOLDMLKNASVRIPT-----LPAYAQAATWHLNLLKH 216
Qy 239 GAELADEWNADIHPSQIEPNAGTSDDYK--LLKENIPKYSNYCANTYREGINKLRNPNM 297
Db 217 AATYNIW---LQNOGINPSTFNSNYQGVYKREKIQYETDYCIQTYNAGLTMTRTNTA 273
Qy 298 RWSIFNRYRMTTIVLDTIAQSFYDIKRYKDSIGRIGGIGKTBELTREIYVTEINFRLT 357
Db 274 TWMYNTYRLMTLTLVLDLIAIFPNYDPEKYP1-----GVKSLTREVY-TNVNSDTER 326
Qy 358 YLETOPNLAIMYNTLRSGLEFLFSLDELIFVTXN-----ETY-----GNRLVGIANRN 406
Db 327 -----TITELNGLTRNP-TLFTWINGQFRYTRNSRDILDPYDIFSGTGNQMA----- 373
Qy 407 RSTVATTGTEIYGBERTG---PPTTKTLIPESY---KVSIVTDROVTPSPFPNIYFT 459
Db 374 -FTHNDNRNIWGNVGHIIISQTSKVPFPRKPKDKVEIVHRE-----YSD 422
Qy 460 INQIELYLNNSPKLTYSAGNLSNDKTTTDFPVPVKOCKPIINPNCLPSYNSYSHIL 519
Db 423 IIVEMIFPSNS-SEVFRYSNSTIENNYKRTDSYMIKQTKW-----NKSEYHTL 471
Qy 520 SQFSLFNYSYKIGLALNIIYLGALGWTHSSVNRNNAISDKLITMIPAKNSLDTNSKVI 579
Db 472 SYIKTDNYFISV---VRRRRVAFSWTHTSVDFQNTIDLNDITQIHALKALKVSSDSKIV 528
Qy 580 EGPHTGNNVYLOSQGLRITCR-TPNSTOSYIRLRYATNGAGNTLPNISLPIPGVIG 638
Db 529 KGPHTGGDLVILKDS--MDPRVRFKXVSQYQVRIYATNA-----PKTTFVLTGIDT 581
Qy 639 IPPORLNNFTSGTNYN--NLQYDGFYQFPSTV-----TLPLNRNIPFIFRADV 687
Db 582 ISVE-LPSTTSKQPNATDLTADFGYVTFPRTPVNTKTFEGEDTLLMT-----LYGTPNH 635
Qy 688 SNSLIIDKIEFIPITSVVRNREKQKLETTQTKTINFTFTH 729
Db 636 SYNI-YIDKIEFIPITQSVDLTEKTEKQKIVNDLFVNN 676
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RESULT 14  
AAR14374

ID AAR14374 standard; protein; 675 AA.

XX AAR14374;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 04-FEB-1992 (first entry)

XX Dipteran active toxin.

XX Insecticide; B.t; crystal; delta endotoxin; cryIVC.

XX Bacillus thuringiensis serovar morrisoni.

XX EP457498-A.

XX 21-NOV-1991.

XX 09-MAY-1991; 91EP-00304180.

XX 15-MAY-1990; 90US-00524255.

PR 01-OCT-1990; 90US-00590903.

XX (MYCO ) MYCOGEN CORP.

XX Sick AJ;

XX WPI; 1991-341902/47.

DR N-PSDB; AAQ14670.

XX Bacillus thuringiensis genes encoding diptera-active toxins - and transformed microbes used to control insects in various environments.

PS Claim 3; Page 15; 20pp; English.

XX The sequence was deduced from the DNA sequence obt'd. from plasmid pMVC1636 which was isolated from a genomic library prep'd. from DNA from B.t. PS71M3 [from B.t. PS71M3-69 (NRRL B-18515)]. It is related to the cryIVC toxins from B.t. var. israelensis. The protein has a mol. wt. of 77 kD. Microorganisms transformed with the DNA may be administered to dipteran insects or their environments, the expressed toxins acting as an insecticide. See also AAR14373. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 675 AA;

Query Match 23.0%; Score 899; DB 2; Length 675;

Best Local Similarity 33.0%; Pred. No. 7.9e-63;

Matches 251; Conservative 114; Mismatches 268; Indels 128; Gaps 32;

Qy 5 NNNVEYIIDSKNLSYPSNRNIDHSRYPTNNPNQPLQNTNYKEWLNMCQGNTOYQDNFET 64

Db 6 NKNEYEIFNAPSNNGFSKNN--YSRYPLANKPNQPLKNTNYKQWLNVCQDNQOQYGNNA 63

Qy 65 PASADTTAAVSAGTIIVSGTLTLAGIGLTSISGPIIGIICAIISFGTLITVFWPAGEQDKT 124

Db 64 FVSSETIVGSAGIIVVGTMLG-----AFAAP--VLAAGIISFGTLPIFW-QGSDPAN 114

Qy 125 VWTQFIKMGEIFVDTPLTE---SIKQLKLTLEGFROILOSNTALDDWRKLEQAPGL 181

Db 115 VWQDLLNIG---GRPIQIEDKNIINVLTSIVTPIKNQLDKYQEFFDKWEPAR----- 163

Qy 182 PPSALQQAALTUKIRENVHN---DFIREIPGQLETYKTLPIYAQAANFHLNLLQ 238

Db 164 --THANAKAVHDLFTTLEPIIDKOLDMLKNASVRIPT-----LPAYAQAATWHLNLLKH 216

Qy 239 GAELADEWNADIHPSQIEPNAGTSDDYK--LLKENIPKYSNYCANTYREGINKLRNPNM 297

Db 217 AATYNIW---LQNOGINPSTFNSNYQGVYKREKIQYETDYCIQTYNAGLTMTRTNTA 273



Db 529 KGPGHTGGDLVILKDS--MDFRVRFLKNVSRQYQVRIRATNA-----PKTTVFLTGIDT 581  
Qy 639 IPPQRLNNTFSGTNYN--NLQYGDGFGYFQPPSTV-----TLPLNRNIPFIENRADV 687  
Db 582 ISVE-LPSTTSRQNPATDLTYADFGYVTFPRTVPNKTPEGEDTLLMT-----LYGTPNH 635  
Qy 688 SNSILIIDKIEPIPTSSVRQNRKQKLETIQTKINTFFTN 728  
Db 636 SYNI-YIDKIEPIPTQSVLDYTEKQNIKTQKIVNDLFVN 675

Search completed: December 15, 2005, 10:50:59  
Job time : 194 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:44:23 ; Search time 232 Seconds  
(without alignments)  
2262.556 Million cell updates/sec

Title: US-10-782-570-2

Perfect score: 3906

Sequence: 1 MNQNNNEYIIDSKNLSYP.....FFTNHTKNTLNIAZNYDID 744

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1158	29.6	1180	1 CR4AA_BACTI	P16480 bacillus th
2	1158	29.6	1180	2 Q7AL67_BACTI	Q7AL67 bacillus th
3	906.5	23.2	1128	2 Q9FDC0_BACTF	Q9FDC0 bacillus th
4	901	23.1	1109	1 C28AA_BACTF	Q9x682 bacillus th
5	897	23.0	675	1 C10AA_BACTI	P09662 bacillus th
6	897	23.0	675	2 Q8KNV2_BACTI	Q8KNV2 bacillus th
7	843	21.6	650	2 Q8VNX2_BACTV	Q8VNX2 bacillus th
8	819	21.0	1136	1 CR4BA_BACTI	P05519 bacillus th
9	819	21.0	1136	2 Q7AL72_BACTI	Q7AL72 bacillus th
10	802	20.5	688	2 Q8VNX1_BACTV	Q8VNX1 bacillus th
11	796	20.4	683	2 Q75VA2_BACTE	Q75VA2 bacillus th
12	791.5	20.3	1169	1 CR8BA_BACUK	Q45705 bacillus th
13	785.5	19.3	688	2 Q8W7N9_BACTU	Q8W7N9 bacillus th
14	712.5	18.2	1169	2 Q56B08_BACTU	Q56B08 bacillus th
15	710	18.2	659	1 P17969_BACTU	P17969 bacillus th
16	709.5	18.2	682	1 C19BA_BACTU	O86170 bacillus th
17	703	18.0	829	2 Q8BE06_BACTU	Q8BE06 bacillus th
18	695	17.8	652	1 CR3BB_BACTU	Q06117 bacillus th
19	693	17.7	1138	1 CR7AB_BACUK	Q45708 bacillus th
20	692	17.7	1138	1 CR7AA_BACTU	Q03749 bacillus th
21	690	17.7	825	2 Q8BE09_BACTU	Q8BE09 bacillus th
22	689	17.6	648	1 C19AA_BACTJ	Q32307 bacillus th
23	687	17.6	660	2 Q8R0U6_BACTA	Q8R0U6 bacillus th
24	686.5	17.6	1236	2 Q339T3_BACTU	Q339T3 bacillus th
25	684	17.5	1280	2 Q8VUK9_BACTU	Q8VUK9 bacillus th
26	681.5	17.4	1157	1 CR8KA_BACTU	Q45704 bacillus th
27	676	17.3	1160	1 CR8CA_BACTP	Q45706 bacillus th
28	676	17.3	1160	2 Q6R2R6_BACTU	Q6R2R6 bacillus th
29	665	17.0	1138	1 CR7AB_BACUA	Q45707 bacillus th
30	666	16.9	686	2 Q75Q05_BACTE	Q75Q05 bacillus th
31	659.5	16.9	1157	1 CR9CA_BACTO	Q45733 bacillus th

32	658.5	16.9	1163	2 Q5XLA8_BACTP	Q5XLA8 bacillus th
33	656	16.8	1169	1 CR9DA_BACTP	Q06014 bacillus th
34	640.5	16.4	1144	2 Q8KZL7_BACTG	Q8KZL7 bacillus th
35	639	16.4	1154	2 Q6QAN9_BACTG	Q6QAN9 bacillus th
36	635	16.3	1254	2 Q8VULO_BACTU	Q8VULO bacillus th
37	630	16.1	826	1 C27AA_BACUH	Q9E597 bacillus th
38	629	16.1	1150	1 CR9EA_BACTA	Q9ZNL9 bacillus th
39	629	16.1	1150	2 Q7IRP4_BACTU	Q7IRP4 bacillus th
40	627.5	16.1	1231	2 Q8KNY2_BACTU	Q8KNY2 bacillus th
41	620.5	15.9	644	1 CR3AA_BACTD	P0A381 bacillus th
42	620.5	15.9	644	1 CR3AA_BACTM	P0A380 bacillus th
43	620.5	15.9	644	1 CR3AA_BACTT	P0A379 bacillus th
44	620.5	15.9	652	2 Q9S6N9_BACTU	Q9S6N9 bacillus th
45	620.5	15.9	1231	1 CR1BD_BACTZ	Q9ZAZ5 bacillus th

#### ALIGNMENTS

##### RESULT 1

ID	CR4AA_BACTI	STANDARD;	PRT;	1180 AA.
AC	P16480;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Pesticidal crystal protein cry4Aa (Insecticidal delta-endotoxin CryIVA(a)) (Crystalline entomocidal protoxin) (135 kDa crystal protein).			
GN	Name=cry4Aa; Synonyms=cryIVA(a), isrH4;			
OS	Bacillus thuringiensis subsp. israelensis.			
OG	Plasmid 72 Kb.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;			
OC	Bacillus cereus group.			
OX	NCBI_TaxID=1430;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Sen K., Honda G., Koyama N., Nishida M., Sakai H., Himeno M., Komano T.;			
RT	"Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes of Bacillus thuringiensis var. israelensis.";			
RL	Agric. Biol. Chem. 52:873-878(1988).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=88015571; PubMed=2821500;			
RA	Ward E.S., Ellar D.J.;			
RT	"Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding a 130 kDa delta-endotoxin.";			
RL	Nucleic Acids Res. 15:7195-7195(1987).			
RN	[3]			
RP	MUTAGENESIS STUDIES.			
RX	MEDLINE=94307434; PubMed=7913448; DOI=10.1016/0014-5793(94)00604-0;			
RA	Nishimoto T., Yoshieue H., Ihara K., Sakai H., Komano T.;			
RT	"Functional analysis of block 5, one of the highly conserved amino acid sequences in the 130-kDa CryIVA protein produced by Bacillus thuringiensis subsp. israelensis.";			
RL	FEBS Lett. 348:249-254(1994).			
CC	-1- FUNCTION: Promotes colloidomotic lysis by binding to the midgut epithelial cells of insects.			
CC	-1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.			
CC	-1- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.			
CC	-1- MISCELLANEOUS: Diverse amino acid mutations in sequence block 667-676 have no direct effect on the insecticidal activity but alter the structural stability of the toxin protein molecule.			
CC	-1- SIMILARITY: Belongs to the delta endotoxin family.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not			







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Db 472 SYIKTDNYIFSV---VRERRVAFSWTHTSVDFQNTIDLDNITQIHAKALKVSSDSKIV 528
Qy 580 EGPCHTGNLYVLSQGRLEITCR--TPNSTQSYVIRLYATNGAGNTLPNLSLTIPGVIG 638
Db 529 KGPCHTGGDLVILKDS--MDPRVFLKNVSRQVRIYATNA-----PKTTVLTGIDT 581
Qy 639 IPPORLANTFSGTNYN--NLQYGDGFGYFQFPSTV-----TLPLNRNIPFPFNADV 687
Db 582 ISVE-LPSTTSRQPNATDLTYADFGVYTPRTVPNKTFEGEDLLMT-----LYGTPNH 635
Qy 688 SNSLIIDKIEFIPITSSVRQNRKQKLETTQTQKINTFFTN 728
Db 636 SYNI-YIDKIEFIPITQSVLDYTEKQIEKTKIVNDLFVN 675

RESULT 6
Q8KNV2 BACTI
ID Q8KNV2 BACTI PRELIMINARY; PRT; 675 AA.
AC Q8KNV2
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pesticidal crystal protein cry10AA.
GN Name=cry10AA; Synonym=cryIVC, cryXA(A), pBt047;
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1430;
RN NUCLEOTIDE SEQUENCE
RP MEDLINE=22235415; PubMed=12324359;
RX DOI=10.1128/AEM.68.10.5082-5095.2002;
RA Berry C., O'Neil S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A.,
RA Harris D., Zaritsky A., Parkhill J.;
RT "Complete sequence and organisation of pBtoxis, the toxin-coding
RT plasmid of Bacillus thuringiensis subsp. israelensis.";
RL Appl. Environ. Microbiol. 68:5082-5095(2002).
DR EMBL; AL731825; CAD30098.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 675 AA; 77759 MW; 4EB0B51AA0372FF1 CRC64;

Query Match 23.0%; Score 897; DB 2; Length 675;
Best Local Similarity 33.0%; Pred. No. 2.1e-48;
Matches 251; Conservative 114; Mismatches 268; Indels 128; Gaps 32;

Qy 5 NNNYEIIDSKNLSYPNRRNIDHSRYPTNNPQNTNYKEWLNMCQGNQYQDNFET 64
Db 6 NKNYEIFNAPSNGFSKSN--YSRYPANKPNQPLKNTNYKWLNVQDNQYQGNAGN 63
Qy 65 FASADTTAASAGTIIVSGTLGAGTSGTSGPTGIGAIISFGTLITVFWPAGEQDKT 124
Db 64 FASSETTVGSAGTIIVGVTMLG-----AFAAP--VLAAGIISFGTLIPFW-QGSDPAN 114
Qy 125 VWTQFIKNGEIVFDTPLTE---SIKQLKLTQLEGFRLOLQSYNTALDWRKLRQLAPGL 181
Db 115 VWQDLNIG-----GRPTQIEDKNVILNVLTSIVTIKQLDKYQFFDKNEPAR----- 163
Qy 182 PPSSALQQAALTKIRFENVHN---DFIREIPGQLEYTKTLPIYAQAANFHLNLLQ 238
Db 164 --THANAKAVHDLFTTLEPIIDKDLMLKNNASVRIPT-----LPAYAQIATWHLNLLKH 216
Qy 239 GAELADFNADIHPSQIEPNAGTSDDYK--LLKENIPKSYNCANTREGLNKLNPNM 297
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Db 217 AATYNTIW---LQOQGNPSTFNSNYYQGYLKRKIOEYTDYCIQTNTAGTMTIRWTNA 273
Qy 298 RWSIFNDYRYMTITVLDTIAQFSFYDIKRYKDSIGRIGIKTELTREIYTTETINFDRLT 357
Db 274 TNNYNTYRLTEWLTVLDLIAIPNYPDEKPI-----GVKSELIREVY--TNVNSDFTF 326
Qy 358 YLSIQPNLAIMEVNLTRSGRLFSPLDELIFYKN-----ETY-----GNRLVGIANRN 406
Db 327 -----TITLENGLTENP--TLFTWINQGRFYTRNSRDILDPPYDIFSFTGNQMA----- 373
Qy 407 RSTVATTGTIIIGERTG---PPTTKLIPESY---KSVITDROVTPSPFPNIFYFT 459
Db 374 -FHTNDRNIINGAVHGNISQDTSKVFPFYRNKPKIDKVEIVHRE-----YSD 422
Qy 460 INQIELYLNNSPNKLTYSAGNLSNDKKTDFQPVVKCKPFIENPCLPSNYSYSHIL 519
Db 423 IIVEMIFPNS-SEVPFYSNSTIENNYKRTDSYMIKQTKW-----NKEYGHTL 471
Qy 520 SQFSLFNYSYKIGLALNLYTGALGTHSSVNRNNAISDKIITMIPAIGNSLDTNSKVI 579
Db 472 SYIKTDNYIFSV---VRERRVAFSWTHTSVDFQNTIDLDNITQIHAKALKVSSDSKIV 528
Qy 580 EGPCHTGNLYVLSQGRLEITCR--TPNSTQSYVIRLYATNGAGNTLPNLSLTIPGVIG 638
Db 529 KGPCHTGGDLVILKDS--MDPRVFLKNVSRQVRIYATNA-----PKTTVLTGIDT 581
Qy 639 IPPORLANTFSGTNYN--NLQYGDGFGYFQFPSTV-----TLPLNRNIPFPFNADV 687
Db 582 ISVE-LPSTTSRQPNATDLTYADFGVYTPRTVPNKTFEGEDLLMT-----LYGTPNH 635
Qy 688 SNSLIIDKIEFIPITSSVRQNRKQKLETTQTQKINTFFTN 728
Db 636 SYNI-YIDKIEFIPITQSVLDYTEKQIEKTKIVNDLFVN 675

RESULT 7
Q8VNX2 BACTV
ID Q8VNX2 BACTV PRELIMINARY; PRT; 650 AA.
AC Q8VNX2
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry29Aa protein.
GN Name=cry29Aa;
OS Bacillus thuringiensis (subsp. medellin).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=79672;
RN NUCLEOTIDE SEQUENCE.
RP Delecluse A., Orduz S.;
RL Submitted (DDBJ/EMBL/GenBank/DBJ databases.
EMBL; AJ251977; CAC80985.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 650 AA; 74435 MW; D0CB846377CC517B CRC64;

Query Match 21.6%; Score 843; DB 2; Length 650;
Best Local Similarity 32.4%; Pred. No. 5.5e-45;
Matches 239; Conservative 126; Mismatches 276; Indels 96; Gaps 26;

Qy 1 MNQ-NNNVEIIDSKNLSYPNRRNIDHSRYPTNNPQNTNYKEWLNMC--QGNQY 57
Db 1 MNSFQNKNEYILNAP--SSISIPNNYSKYPIANTLNQMTQNTYKDWNTMCAIDNNLK 58
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QY	58	YGDNFETASADTIAAASAGTIVSGTLGAGIGGLTISGPIGIIIGAIISFGTLITVFWP	117	RP	NUCLEOTIDE SEQUENCE.
Db	59	SINPFENLQNSVLGFAITAAIASLSSAPITGTSIACTAJAAI-----IPILMP	111	RC	STRAIN=402-72;
QY	118	AGBQDKTVVTFQIKMGEIFVDVTLPTESIKQKQLQTLGEGFRQILQSNTALDDWRKLRLQ	177	RX	MEDLINE=88185334; PubMed=28333395;
Db	112	S--QENNLDPKLLAISATLYSQDQVRREDALTRLLESLKDSVKYPENAFTFIN----	164	RA	Chungjatupornchai W., Hoeft H., Seurinck J., Angsuthanasombat C., Vaeck M.;
QY	178	APGLPSSALQQAALTLKIFENVHNDFREIPGFQLETKYTLTLLPIYAQAAPHNLQ	237	RA	"Common features of Bacillus thuringiensis toxins specific for Diptera and Lepidoptera.";
Db	165	-----NPNST---NTTVTRERFQEVNGRFVSGMAFFRAKNYEPILLSTYAAQARLLHLR	217	RT	Eur. J. Biochem. 173:9-16(1988).
QY	238	QGAELADEWNADTHPSQIEPNAGTSDDYKLLKENIPKYSNCANTYREGNKLREPNM	297	RL	[3]
Db	218	DGITYAEKMWLSRGDDM-----PGDLLYKEFNKYCNEYIEHCWKYNBSLSLKS-VGA	271	RN	NUCLEOTIDE SEQUENCE.
QY	298	RWSIFNDYRYMTITVLDITIAQFSFYDIKRYKDSIGRIGIKTELREIYTTTEINFDRLT	357	RA	Komano T.;
Db	272	NWLEYNQRTFLTASVLDVLSLSSVDPRLYKERLS-----VEILTRKLYTDPINYHGI	326	RA	"Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes of Bacillus thuringiensis var. israelensis.";
QY	358	YLSIQPNLAMEYNLTRSGURLSFLDELIPYKNETYGNRLVGIANRNSTVATTGTEI	417	RL	Agric. Biol. Chem. 52:873-878(1988).
Db	327	SLEADES---KYLEPT---LFTQLYTLTFYS-NIFY--NYMGHTN---TYRYSPOK	372	RN	NUCLEOTIDE SEQUENCE.
QY	418	IYGERGPTTKTLIPESY--KVSIVTDQVTPTSFPFNIYETINQIELYLNNSPNKL	475	RX	MEDLINE=88329719; PubMed=2901387; DOI=10.1016/0378-1119(88)90229-6;
Db	373	IFAEKFGKQS-----SYDKVPVI-----PNDKSIYKIRAYDNHNGLFNV	414	RA	Angsuthanasombat C., Chungjatupornchai W., Kertbundit S., Luxanani P., Sattasatian C., Wilairat P., Panyim S.;
QY	476	TSAGGNLSNDKKTDFQFPVKDKCKPIINPCLPSVNSYSHLSOFSLFNYKYKIGLAL	535	RT	"Cloning and expression of 130-kd mosquito-larvicidal delta-endotoxin gene of Bacillus thuringiensis var. israelensis in Escherichia coli.";
Db	415	MYGFWGDKQD---IQKIIGSGSTEIYKNC-----THRLADVISHDLDEK----	458	RL	Mol. Gen. Genet. 208:384-389(1987).
QY	536	NILYTGALGHTHSVNRNNAISKITMTIPAIGNSLDTNSKVIPEGHTGMLVYLSQ	595	CC	-I- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut epithelial cells of mosquitoes.
Db	459	NKCYSPA--WTSTISLENIKNDIITQIPAVKAYQLGVQSVIKGPGHTGGDLNLKSN	516	CC	-I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
QY	596	GRLEITCR-TPNSTQSYVIRLVATGAGNTLNPISITIPGVIGIPQR--LNNTPSGTN	652	CC	-I- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
Db	517	DYRISCOHLSNVTKYFVRIRATNGSLNTRPIIMITIP---GMTPOGMVLNDFSGTG	573	CC	-I- SIMILARITY: Belongs to the delta endotoxin family.
QY	653	YNNLOQDFGYFQFPSTVTPLNRPNPFIPFNADV-SNSILIDKIEFIPITSSVRQNR	711	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
Db	574	YSNLEQNFQYKEFLKEVTLNPNQISLTLNRSDQNSLILLDRIEFLPITPSIRKSKE	633	DR	EMBL; X07082; CAA30114.1; -; Genomic DNA.
QY	712	KQKLEIQTQKINTFFTN 728		DR	EMBL; X05692; CAA29174.1; -; Genomic DNA.
Db	634	QONLEKNQKTVNKLFFN 650		DR	EMBL; D00247; BAA00178.1; -; Genomic DNA.
				DR	EMBL; M20242; AAA22337.1; -; Genomic DNA.
				DR	EMBL; X07423; CAA30312.1; -; Genomic DNA.
				DR	PIR; S00398; USBS91.
				DR	PDB; 1W99; X-ray; A=84-641.
				DR	InterPro; IPR001178; Endotoxin.
				DR	InterPro; IPR005638; endotoxin.C.
				DR	InterPro; IPR005639; endotoxin_N.
				DR	Pfam; PF03944; Endotoxin_C; 1.
				DR	Pfam; PF00555; Endotoxin_M; 1.
				DR	Pfam; PF03945; Endotoxin_N; 1.
				DR	3D-structure; Plasmid; Sporulation; Toxin.
				FT	CONFLICT 51 51 V -> D (in Ref. 4).
				FT	CONFLICT 65 65 T -> S (in Ref. 4).
				FT	CONFLICT 193 201 LINAQEWSL -> PHKCTRMVY (in Ref. 4).
				FT	CONFLICT 203 204 RS -> C (in Ref. 3).
				FT	CONFLICT 205 206 AG -> C (in Ref. 4).
				FT	CONFLICT 205 205 A -> R (in Ref. 1).
				FT	CONFLICT 272 272 Y -> L (in Ref. 3).
				FT	CONFLICT 325 325 D -> Y (in Ref. 3).
				FT	CONFLICT 364 401 FGSNTHQQLNSNVKYSITDTSFSPNRVTKMDFYKI -> LVQYILKFNPLILVILKLSQLAPLLELQKWISTKF (in Ref. 4).
				FT	CONFLICT 467 467 K -> N (in Ref. 4).







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QY 704 SSVQRNREKQLEIQTQKINTFTNHTKNTLNIETATNYDID 744
Db 635 QSVLDETENQLESEREVNALTNDKALNIGTTDID 675

RESULT 10
Q8VNX1_BACTV
ID Q8VNX1_BACTV PRELIMINARY; PRT; 688 AA.
AC Q8VNX1;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Cry30Aa protein.
GN Name=cry30Aa;
OS Bacillus thuringiensis (subsp. medellin).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=79672;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Delecluse A., Orduz S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251978; CAC80986.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 688 AA; 77844 MW; 7E0D57085BD7B3A9 CRC64;

Query Match 20.5%; Score 802; DB 2; Length 688;
Best Local Similarity 32.4%; Pred. No. 2.4e-42;
Matches 246; Conservative 109; Mismatches 274; Indels 130; Gaps 31;

QY 1 MNQ-NNNNEYIID-SKNLSYPSNRNIDHSRYPTNNPQNPLQNTNYKEWLNMCQNTQY 58
Db 1 MNSYENKNEYIILDTQSKNSMNR---YSKYPLTNNPKVPLQNTNYKWLNNCQITPL 57
QY 59 GDNFETPASADTTAAVSAGTIVSGTLGAGTGSISGPIGIGAIISFGTLITVFWPA 118
Db 58 CTPIDTDSKLVAITKIGAI-----FKSMPPGPGAAVGLVLKSFSTIIPILWP- 105
QY 119 GEODKT-VMTQFIKWG-EIFVDTPLTESIK-----QLKLTLEGFRQILQSYNTALDDW 170
Db 106 --NDKTPIWKEFTKQGLQFLRPELGDAIEIIGNDVQAESYLE---IMMRDPENKPAW 160
QY 171 RLKRLQAPGLPSSALQQAALTLKIRFENVHNDFIREIPGQL-ETYKTLILLPIYAQA 229
Db 161 E-----SNRTRNAIAVTAFTSTVNTQILKRFLLIAENRPAFLNLAQTA 208
QY 230 NFHLNLQQAELADEWNAIHPSQIEPNAGTSDDYKLLKENIPKSYNCANTYREGN 289
Db 209 NIDLILYQSGSVYGDKWADVADINNRSTP--FSSKDYYSQSLGKIKDYNTYCAETYSNLT 266
QY 290 KLARNEPNRWSIENDRYVNTITVLDITIAQSFVDIKRYKDSIGRIGGIKTELTRITYT 349
Db 267 ILKNKPHIQNDIYNRYRREAILGALDLVALFPNDICIYPTQ-----TRTELTRKYMP 320
QY 350 EINFDRILTYLEI--QPNLAIMEYNLTRSGLRFLSFDELIFYTKNETYG-----NRLVGI 402
Db 321 SF-----YLQAQQRDIETVENQLTHPP-SLFTWLNELNLYTIRERPNVQLVASLSGL 373
QY 403 ANNRSTY-ATTGTEIYGE-RTGPPPTKTLIPFESYKVSIVTDQVTPSPFNPTFTI 460
Db 374 QATSRYQTNTTISNPVQGPVREGTPTKISLANYYIKLPMYSQVRPNDCLPISG----I 429
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QY 461 NOIELYLN-----SPSNKL-TYSAGN-----LSNDKTKTDFQFPVKDC 500
Db 430 NEMSPYRSDYYCAGCAPHYVSAGESPTNVIKTYNGQNALISND----- 475
QY 501 KPINPNCPLPSYNSHILSQSFLFNYSYKIGLALNILYTGALGHTHSSVNRNNAISDKI 560
Db 476 -----ISINETSHILSDIKM-NYSRTGGVPLYDFGYSFAWHTTSDVDNLIVPNR 525
QY 561 ITMIPAIGNSLDTNSKVIIEGPHGTGGNLVYL-----SQGRLEITCRPTNST---QSYVI 613
Db 526 ITQIPAVKAYSLTSPARVIVGEGHTGGDLVALLNSGTQSGTMOIQCKTSGTGPGRQYGL 585
QY 614 RLRYATNGAGNTLPNISLTIPGIVIGIPQRLNNTFSGTNY---NNLQYGDGFGYFOPPS-- 668
Db 586 RMRYAANSFTV--SLSYTLGQTGTSFVTEFTSRNNIIPTDLKTEEFKYKDYLOLI 643
QY 669 TVTLPLNRNIPPIFNRA-DVNSIILIDKIEFIPITSSV 706
Db 644 TMTLPANTITITSMQOATGLNQLNQLIIDRIEFYPMQGV 682

RESULT 11
Q75VA2_BACTE
ID Q75VA2_BACTE PRELIMINARY; PRT; 683 AA.
AC Q75VA2;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Putative mosquitoicidal toxin.
GN Name=cry30Aa like;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1436;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=INA288;
RA Ikeya T., Yamaya K., Ito T., Sahara K., Bando H., Asano S.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB125059; BAD00052.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 683 AA; 77438 MW; 488B477B876BFDCA CRC64;

Query Match 20.4%; Score 796; DB 2; Length 683;
Best Local Similarity 31.4%; Pred. No. 5.8e-42;
Matches 245; Conservative 107; Mismatches 264; Indels 164; Gaps 32;

QY 8 EYEIDSKNLSYPSNRNIDHSRYPTNNPQNPLQNTNYKEWLNMCQNTQYGDNFTFAS 67
Db 9 EYEILDA--LPNYSNNVAYSRYPLANNPQVPLQNTSYKDWLNMCO-----TINP 56
QY 68 ADT-----IAAVSAGTIVSGTLGAGTGSISGPIGIGAIISFGTLITVFWPAGEQD 122
Db 57 LCTPINIDISLAAASIAVVGSI-----LIPGGEALGFVLGTFSTILPILNPG-- 108
QY 123 KTVWTQFIKWG-EIFVDTPLTESIKQLKLTLEGFRQI---LQSYNTALDDWRKLRLOA 178
Db 109 TKIWTDFAEERGLQFLRPELGQDAIELYTVGKSGYNALKNRMENFEQAFTKKK----- 161
QY 179 PGLPSSALQQAALTLKIR-FENVNDFTIREIPGQLE-TYKTLILLPIYAQAANFILNLL 236
Db 162 -GNRTSRNAEQV-----IRDFDSVRDKVIDLKNYMINPENKPAFINLYAQTANIDLILY 215
```

QY 237 OQGAELADENADHPQIEPNAGTSDYYKLLKENIPKYSNYCANYTYREGINKLRNEPN 296  
 DB 216 QRGAVYGDWKEKINGS-ISPFG-SKDYVESLTKIEEYNYCAETVRSNLKKNKPN 273  
 QY 297 MRWSIFNDYRYMTITVLTDAQSFYDIKRYKDSIGRIGIKTELREIYVTEINFDR 356  
 DB 274 ISWYTKYREAVTGALDVALFPNDMLHP-----AATKTELTKYIMPSFGLOOS 327  
 QY 357 TYLEIQPNLAIMEYNLTRSGRLFSFLDELIFYTKNETYG-----NRLVGIANRNRSTYA 411  
 DB 328 NYFQ---SLEGLENALTHPP-SLFTWLNELNLYTVRENFNPALQVSSLSGLQASRYTON 383  
 QY 412 TTGTE-IYIGERTGPTTKTILIPESYKSVIVDRQVTPSPFFNIYFTINQIELY---L 467  
 DB 384 PTILNDPAQGVNRGTSTQIGLNNLFVYKLSMSQYHHPNDCSSIAAG-----ISDMTFYKSDY 439  
 QY 468 NNSPSNKLTYSAGNLSNKKTTDFQFPVKDKCPIN-----NCLPSVNSYS-----H 517  
 DB 440 NGNASATQYQAGRTNN-----VINTFNGQKASSNNSIKQTKH 482  
 QY 518 ILSQFSL-----FNYSYKIGLALNLYTGALGTHSSVNRNNAISDKIITMI 564  
 DB 483 ILSDKMIYPTGMYQVYDFGYSF-----AMTHSVDPNDLIVPNRITQI 528  
 QY 565 PAIKGNSLDNWSKIEGPGHTGGLNVLVLOSQRLEICTRPNSTQSYIIRURYATNAGN 624  
 DB 529 PAVKALGISTDSKVVGPFVFGDGLLLKLOQTIRI--KTDHANTRYKIRVRYASN--AN 584  
 QY 625 T-----LPN-LSITPCVIGIPQRLNNTFSGTNVNNLOVDFGYQFPSTVTLPLNRN 677  
 DB 585 TPVLSLQNTLVITFP-----QTITHSTISELQYKQYVTFPG-----624  
 QY 678 IPFIFNRADVNSI-----LIIDKIEPIPTSSVRQNRKQKLETIQKINTFTFN 728  
 DB 625 -EFIMDXPSIDVARGQNDENDWIDRIEPLITQSVLDVTEBQNIKESQKAVNDLFIN 683  
 RESULT 12  
 CR8BA\_BACUK STANDARD; PRT; 1169 AA.  
 AC Q45705;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Pestidicial crystal protein cry8Ba (Insecticidal delta-endotoxin  
 DE CryVIIIB(a)) (Crystalline entomocidal protoxin) (134 kDa crystal  
 DE protein)  
 GN Name=cry8Ba; Synonyms=50C(b), cryVIIIB(a);  
 OS Bacillus thuringiensis subsp. kumamotoensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=132267;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=NRRL B-18746 / PS50C;  
 RA Michaels T.E., Foncerra L., Narva K.E.;  
 RT "Process for controlling scarab pests with Bacillus thuringiensis  
 RT isolates";  
 RL Patent number WO9315206, 05-AUG-1993.  
 CC -1- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 CC epithelial cells of insects. Active on various scarabaeid beetles.  
 CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -1- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC -----; AAA21118.1; -, Genomic DNA.  
 DR HSBP; P07130; 1DLC.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 1169 AA; 133544 MW; 22EEFCF5BD699909 CRC64;  
 Query Match 20.3%; Score 791.5; DB 1; Length 1169;  
 Best Local Similarity 28.0%; Pred. No. 2.3e-41;  
 Matches 217; Conservative 151; Mismatches 237; Indels 109; Gaps 28;  
 QY 1 MNQNNNEYEIIIDSKNLSYPSNRNIDHSRYPTNNPQPLQNTNYKEMLANCOGN-TOYG 59  
 DB 1 MSPNNQNEYEIIIDATPSTSVSN---DSNRYPFANEPTNALQNMDYKDYKMGAGNVSEYP 57  
 QY 60 DNFETFASADTIAAVSAGTIVSGTLGAGIGLTSISGPIGIIIGAIISFGTLITVFWPAG 119  
 DB 58 GSPFVFLSEQD--AVKAAIDIVGKLLTGLG-----VPFVGPVLSLYTQIDILWPS- 106  
 QY 120 EQDKTVVTQIKGEIIPVDPPLTESIKQLKQLEGPQILQSYNTALDDWRKLRLOAP 179  
 DB 107 -KQKSQWEIEMEQVEELINQKIAEYARKALKSELEGLGNNYQLYLTALKEWKE----- 158  
 QY 180 GLPSSALQAAALTAKIRFENVHDFIREIPGQLEYKTKILLPIYAAQANFHLNLAQOG 239  
 DB 159 --NPNGS--RALRDVRNRFELDSLTQYMPSPRVNTFVFPFLTVYVYTAANLHLLLRDA 214  
 QY 240 AELADENADHPQSIEPNAGTSDYYKLLKENIPKYSNYCANYTYREGINKLRNEPNRW 299  
 DB 215 SIFGEENGL-----STSTNNYNRQMKLTAEYSDHCVKYEYGLAKLKSSAKQW 265  
 QY 300 SIFNDYRYMTITVLTDAQSFYDIKRYKDSIGRIGIKTELREIYVTEINFDRITYL 359  
 DB 266 IDYNQFREMFLAVLDVVALFSNYDTRTYPLA-----TTAQLTREYVT-----DPLGAV 314  
 QY 360 EIOPNL-----ALMEYNLTRSGLR---LFSFLDELIFYTKNETY-GNRLVGIANRNRST 409  
 DB 315 DV-PNIGSWYDKAPSFSEIEKAAIRPHVFDYITGLTVYTKGRSFTSDRYNRYWAGHOIS 373  
 QY 410 YATGTGIEIIGERTGPTTKTL-----IPFESYKV-SIVTDROVTPSPFPNI----- 456  
 DB 374 YKHGTSSTETQMGV--TNQNLQSTNFDFTNVDIYKLSNGAVLZDIVVPGYTYTFEGM 431  
 QY 457 -----YFTINQIEIYLNNSPNKLTYS--AGNLSNDKKTDFQFPVKDKCKPIINPCLPS 511  
 DB 432 PETEFFMVNQL-----NNTKRLTYKPAKDIIDRTDSELELPPESTGQ-----PN 478  
 QY 512 YNSVSHLSQFSLFNYSYKIGLALNLYTGALGTHSSVNRNNAISDKITMIPAIKGN 571  
 DB 479 YESYSHRLGHIT-FIYS-----STSTYVVPFVSWTHRSADLTNTVKSGETIQTIPGKSST 532  
 QY 572 LDYNSKVIIEGPGHTGGLNVLVLOSQ-GRLEITCTRPNSTQSYIIRURYATNAGNLTENIS 630  
 DB 533 IGRNTYIKRGYTGGLDVALTDRIKSCFQMFIPES-QRFRIRIRVASNETS-----Y 585  
 QY 631 LTPGVIGIPQRLNNTFSGTNVNNLOVDFGYQFPSTVTLPLNRNIPFIFNRADVNS 690  
 DB 586 ISLYGLNQSGTLKFPNQTSYKNKNENDLTNDFKYIEYPRVISVNASNIIQRLSIGIQTNTN 645  
 QY 691 ILIIDKIEPIPTSSVRQNRKQKLETIQKINTFTFNHTKNTLNIEATNYDID 744  
 DB 646 LFILDRIEFIPVDEYAEATD---LEAAKKAVALFTN-TKDLGQLQPGVTDYEVN 695  
 RESULT 13  
 Q5W7N9\_BACTU  
 ID Q5W7N9\_BACTU PRELIMINARY; PRT; 688 AA.  
 AC Q5W7N9;



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Db 416 TS-----DVQINSISNLASALSTL-----RGVTRAQFHYGSG-----IISVYG----- 456
Qy 488 KTTDFQFPVKDC-----KPIINPCLPSYNSHILSQFSFNYSYK-----IGLAL 535
Db 457 -----QNNVLPOCHQNYNISBELPNQSDPEPTVRSYSHRLSHITSFNSVOLNPNVISLGN 511
Qy 536 NILTGALGHTHSSVNRNNAISDKIITMIPIAKGNSLDTNSKVIEGPGHTGCGNLVYLQSQ 595
Db 512 MPVVV-----WTHRSVDLNTTISDRITQLPAVKASTLGAGAIIVKGPFTGCDVIRRTSV 567
Qy 596 G-----RLEICTRPNSQSYIIRLVATNGAGNTLPNISLTIPGVIGIPQRLNNTFSG 650
Db 568 GDFGTIRVSV-----TGSLTQQRIRPRYA-----STIDPFFVIRG-----G 605
Qy 651 TNYNNLQY-----GDFGYFQFPSTVTLPLNRNIPPIFNRA-DV-----SNSILII 694
Db 606 TTINFRTHMTSSGEESRYESYRTVEP-----STPFNTQSODIIRTSIQGLSGNGEYVL 661
Qy 695 DKIRFIPITSSVRQNRQKLETTQTKINTPFTWHTKNTLMEATNYDID 744
Db 662 DRIEIPVNPNT---REABEDLEDAKCAVAGLFT-RTRDGLQVNTDYQVD 707

RESULT 15
CR3BA_BACTO
ID CR3BA_BACTO STANDARD; PRT; 659 AA.
AC P17969;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal crystal protein cry3Ba (insecticidal delta-endotoxin
DE CryIIIB(a) (Crystalline entomocidal protoxin) (75 kDa crystal
DE protein).
GN Name=cry3Ba; Synonyms=cryIIb, cryIIIB(a);
OS Bacillus thuringiensis subsp. tolworthi;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1442;
RN (1)
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=43F;
RX MEDLINE=90206811; PubMed=2320431;
RA Sick A., Gaertner F.H., Wong A.;
RT "Nucleotide sequence of a coleopteran-active toxin gene from a new
RT isolate of Bacillus thuringiensis subsp. tolworthi.";
RL Nucleic Acids Res. 18:1305-1305(1990).
CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X17123; CAA34983.1; -; Genomic DNA.
CC EMBL; A07234; CAA00645.1; -; Unassigned DNA.
CC PIR; S10228; S10228.
CC HSSP; Q06117; 1J16.
CC SMR; P17969; 72-659.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; Endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
KW

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SQ SEQUENCE 659 AA; 75159 MW; 5A5B214FF84168CA CRC64;
Query Match 18.2%; Score 710; DB 1; Length 659;
Best Local Similarity 28.9%; Pred. No. 1.6e-36;
Matches 217; Conservative 115; Mismatches 270; Indels 148; Gaps 31;
Qy 1 MNQNNNEVEIID-SKULSYSPSRNIDHSPPYNNNQPLONTNYKEWLNKMGCOGTQYG 59
Db 9 MNPNNRSEYDTIKVTPNSELPFN-----HNOYPLADNPNSTLBELNYKEFLRMTADNST-- 62
Qy 60 DNFETPASADTIAAVSAGTIIVSGTLLAGIGGLTSISGPIGIIIGAIISFGTLITVFPFAG 119
Db 63 ----EVLDSSTVKDAVGTSIVSQILGVG-----VFFAGALTSTFYQSFNAIWPS- 110
Qy 120 EQDKTVMTQFIKGEIFVDFTLTESIKQLKQLTLEGFRQILQSYNTALDWRKLRLOAP 179
Db 111 --DADPWKAFMAQVEVLIDKKIEYAKSKALAELOGLQNNFEDYVNALDSWK----- 161
Qy 180 GLPSSALQQAALTLKIRFENVNDPIREIPGQLETYKTLILLPIYAAANFHLNLIQOG 239
Db 162 -APVNLRSRSQDRIRELFQSAESHFERNMSPFAVSKFEVLFLPTYAQAANTHLLLKDA 220
Qy 240 AELADEWNADIHPSQIEPNAGTSD--YYKLLKENIPKYSNYCANTYREGLNKLRNEPN 296
Db 221 QVFGEEWGY-----SSEDIAEYQORQLKLTQQTIDRCVNNYVGLNSLRSTY 268
Qy 297 MRWSIFNDYRRYMTITVLDITIAQFSFYDIKRYKDSIGRIQIKTELTRREIYTTINFDR 356
Db 269 DAWKFNRRPREMTLVLDLIVLFFPYDVRYSK-----GVKTELTRDITFDPI-FTLN 321
Qy 357 TYLEIQNLAIMENVLTRSGRLFSFLDELIFYTK-----NETVGNRLVGLIAR 405
Db 322 ALQEGYGTFFSIIENSIRKP--HLFDYLRGIEFTLRPLPGYSGKDSFYWSGNY---VETR 376
Qy 406 NRSTYATGTETIIVGERTGPTTKTLIPPSYKSVIVTDQV--TPTSPPRN--IYFTIN 461
Db 377 PSIGSNDTIYSPFYGDKSIEPIQK--LSFDQKQVY-----RTIANDIAAFPDGKIYFGVT 430
Qy 462 QIELYLNNSPSNKL---TYSA-----GGNLSNDK---KTTDFQFPVKCKCKPIINPNC 508
Db 431 KVPFSQYDDQKNSTSTQTYDSKRYNGYLGAQDSIDQLPETTD--EPEK----- 478
Qy 509 LPSVNSYSHILSQPSLFNYSYKIGLALNIIYTGALGHTHSSVNRNNAISDKIITMIPIAK 568
Db 479 ----AYSHQLNVAECFLMDRRGTI--PFFT-----WTHRSVDPFNTIDAEKITQLPVVK 527
Qy 569 GNSLDTNSKVIEGPGHTGCGNLVYLQ-----SOGRLIETCRTPNSTQSYIIRLVATNGAGN 624
Db 528 AYALSSGASIIEGPFTGGNLLFLKSSNSIAKPKVTNLNSAALLQRTVRIRIYAST---- 583
Qy 625 TLPNISLTIPGVIGIPQRLNNTFSGTNYNNLQY--GDFGY--FQFPSTVTLPLNRNIPF 680
Db 584 --TNLRLFV-----QNSNDELVIYINKWNIDGLTYQTFDFATS-----NSNMGF 628
Qy 681 IFNRAD-----VNSIILIIIDKIEPIPI 702
Db 629 SGTNDNFIIGAESFVSNEKIIDKIEPIV 658

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Search completed: December 15, 2005, 10:54:56

Job time : 235 secs

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